

**FIGURE 1**

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC  
TGCAGACTAAACCACTATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTTGGTCTGAAGTGGTGGCTGCCATCGTAGG  
ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCTTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCTATTCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCTATGTTAGATCG  
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

**FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902  
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown  
><MW: -1, pI: 8.36, NX(S/T): 1  
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF  
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTTLVFLVELVAAIVGFVFRHEIKNSFKN  
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ  
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA  
 GGAGTCGCGCCCGCCGCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT  
 GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
 TGGGGACGTCGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
 GCCGGGGTAGGCTCTGAAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTAGAAAGAGGGT  
 GTTCCCTCTTTCGGGGGTCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT  
 GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG  
 GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTCC  
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAGAACTGAAACTACCTAAATGATCGTCTTTG  
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
 CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
 CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCAACAGCAACAGGCCGAGAACAGTG  
 CAGTACCCACTGCTGACACAAGGAGCCAACACGGGACCCTGTTGCGCCACCAAGGAGGGGC  
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGGACACACT  
 GGCAGTAATACGGACTCTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
 GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
 CCAAGCCTTGCTGCTCACAGGGCAAAGGAGAATATTTAATGCTCCGCTGATGGCAGAGTAAA  
 TGATAAGATTTGATGTTTTTGCTTGCTGTCTACTTTGTCTGGAAATGTCTAAATGTTTC  
 TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

**FIGURE 4**

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPFRRGPGPEFRKKQNVDGLVLDLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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**FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTTCAGCCCATTGCGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTG  
CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTC**TAG**CATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA  
AAAAAAAAAAAA

**FIGURE 6**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER  
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFRRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85



**FIGURE 8**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT  
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW  
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF  
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVKIEKKLAIWEQLSPDIKQQYGEgyIEKSLD  
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK  
AELANPKAV

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



**FIGURE 9**

GCGGGCTGTTGACGGCGCTGCG**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTCTTGACGCCGCCAGTGGGCGGGGCCCTTGGGCGGTCGCCACCACT  
 GTAGTCATGTACCCACGCCGCCGCCGCCCTCATCGGAGTTCTCTCGGTGACGCTGAG  
 CTTTGGCGGAGAGCTATGACAAACAGCAAGAGTTGGCGGGCGGCGCTCGTGCTGGAGGAAATGGA  
 AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT  
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAACCAGCAAATCCACCCGCTTACCAG  
 CTCCTCAGAAGGGCGACACCGACCTTGAGAACTTACCTGAGATTTCGTACAGAAGACACAA  
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCTGTGGATCCCCGCCGGAAGGAG  
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCTGAGCAGGGCACCGAG  
 CTCCTTCAAGAAGAGCAGAAGTCCCCACCAGCCTCCCTGCCACCGGCCAGGACACAGGG  
 CACACCAGTGCATCTGAACATATCGCCAGAAGGGCGTGATTGACGCTTCTCTGCATGCATGGA  
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT  
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT  
 GAGGAAAGAAATTTGAGGAAGCCAGGAAGTGGGTGTGCGAAGAAGTTACACTTTGAAAAGGACG  
 TGGACGTCACCTGTTTGAAGACAGATCCGCATCCTGGGGGGCTCCTGAGTGCCATACCA  
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC  
 CTTCAGAACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC  
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG  
 GAGCTCTCCCGTCTCACAGGGGATAAGAAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA  
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG  
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGGCCAGAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGTAGAACGCGGCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTG  
 TGGGGGAGCTTGCCACGGCCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTTGCCA  
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCGCCAGCCACATGGAGCTGGCCAGGA  
 GCTCATGGAGACTTGTACAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG  
 TGCATTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG  
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTACAGGGGA  
 CCGCAAATACCAGGACTGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC  
 CCTCGGGTGGCTATTCTTCCATCAACAAATGTCCAGGATCCTCAGAAGCCCCAGCCTAGGGAC  
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCAACCTCTGCCTATCT  
 GGACCCCTGCCT**TAG**GGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCAGAGGCACCTTG  
 CTGGGTCTGTGGCATTTCCTCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGGCCAGGCT  
 CTGAACCTGGCTCTGGGCTCCTCTGCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA  
 GGCCCTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGTGGAGCTCCGCTGCTTCTCTC  
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA  
 GAGGGGGGCTTCGAGGTGTCCCTGTGTAAGGGTGACCGAGTGGACAGCCAGGGTGCAGC  
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA  
 CTCAGAGGCTGAGGCTCCAGGGTGGCTCTGGTGTTTACAAGCTGGACTCAGGATCCTCT  
 CTGGCCGCCCGCAGGGGGCTTGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCT  
 CCAGTGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA

**FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSTFGESYDN  
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE  
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT  
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVPTKPPLPPARTQGTPVHLNY  
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGGLTLIDALDTMWILGLRKEFEEA  
RKWVSKKLHFEKDVDVNLFFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI  
PYSDVNIGTGVAHPPRWTSdstVAEVTsIQLEFRELsRLTGDKKFQEAVEKVtQHihGLSGK  
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT  
HLLRHSEPSKLTfVgELAHGRFSakMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ  
MNRQMETGLSPEIVHfNLYPQPGRRDVEVKPADRHNLlRPETVESLFYLYRVtGDRKYQDWG  
WEILQSFsRfTRVPsGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLfLLFSDDPNLLSLD  
AYVENTEAHPLPIWTPA

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GCGCCGCGTAGGCCCGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
 CGCCTCTCCGCACG**ATGT**TCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
 AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCGTCTTCCACCTGTTTCGTGGC  
 CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
 CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAG  
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACC GCCTGGCAGTGCTGGT  
 GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTCTGA  
 GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
 CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC  
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
 CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAGGGAGCTGGGCTCCAGCTTTTCC  
 GCCCCCTCGGAATCACAACCTGGGTACAAGACATTTGCCACCTGCATGACCCAGCCTGGCGG  
 AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
 AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC  
 CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC  
 AGCT**GA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
 CAAGGCCTCAGGTCGTGGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
 AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
 GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG  
 GGACCCCCCTGCCTTCTGTCTACCCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG  
 TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCTACTCTGACCTCCTTCACGTGCC  
 AGGCCTGTGGGTAGTGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSSLGFFSLLWLQLSCSGDVARAVR  
GQGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKI  
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPPEAGPFHVA  
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDDEFYRRIKGAGLQLFRPSGI  
TTGYKTFRHLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

**FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGCTTAAGAAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
CCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT  
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 14**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFPPSFLCLLPHRPAMTCSQAQ

PRGEGEKVGDG

**Important features:****Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 15**

GGGACCCATGCGGCGGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAAG  
 GAGCATGTCCGCGCCGGGAAGGCCCGTCTCCGCGCCGCATAAGGCTCCGGTCCGCGCTGG  
 GCCCGCGCGCGCTCTCTGCCGCGCGGGCTCCGGGCGGCCCCGTAGGCCAGTGCGCCGCCG  
 CTCGCCCCGAGGCCCGGCCCGCAGC**ATGG**AGCCACCCGACGCCGGCGGGGCCGCGCGCA  
 GCCGCGCGTGTGTGCGCGCTCTCGCTGTTAGCGCTGCTCGCGTGTCTGGGAGGCGCGCGG  
 GCGGCGGCGCGCGCGCGCTGCCGCGCGGTGCAAGCAGCATGGGCGGCCCCGAGGGGCTGGC  
 AGGGCGGCGGCGCGCGGAGGGCAAGGTGGTGTGCAGCAGCCTGGAAGTCTCGCGAGGTCTCT  
 GCCCCAGATACTCTGCCAACCACGACGGTCAACCTGATTCTGAGTAACAATAAGATATCCG  
 AGCTGAAGAATGGCTCATTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT  
 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGACTGTCATCTCTAAAAAGATTGGATCT  
 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTCGAGGACTCACCATCTGGTTC  
 GGCTAAACCTTTCGGGAATTTGTTTCTCATTATCTCAAGGAACCTTTTGATATCTTGCG  
 TCATTACGGTCTTTGGAATCCAGACTGAGTATCTTTGTGTGACTGTAACATACCTGTGGAT  
 GCATCGCTGGGTAAAGGAGAAGAACATACGGTACGGGATACAGGTGTGTTTATCCTAAGT  
 CACTGCAGGCCCAACCAGTCAAGCGGTGAAGCAGGAGCTGTTGACATGCGACCTCCGCTT  
 GAATTGCCGCTCTTTTACATGACTCCATCTCATCGCCAAGTGTGTTGAAGGAGACAGCCT  
 TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAGGATG  
 GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGTAAGAACATGATTACACAAC  
 TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTCAGGCTGGATCTACTGGAAATTG  
 GGGCTGTCTGTCCAGACCAACGTGGGAATAATACGAGGACTGTGGATATTGGTATTAG  
 AGAGTCTGACACGACTGTCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
 CCCAGAACATTGCCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG  
 GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
 TTTGGGCAGATGATGATTATCTCGCTGTGATGCAATGATGTCTAGAGTCTTTAT  
 ATGTTTAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC  
 TTACACTGTGGAAGCAGCCAACTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA  
 TTGAAAAATTTGGAAGATTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT  
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC  
 TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCAATCAAGTCT  
 ACTGGCTTACGGGGATGACCTGTACCGTGTTCAGAAAAGTGGCAGCCTCTGATCTGACAGG  
 ACTTTCGATTATGGGAGGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT  
 GCAATGTTTCAAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATT  
 AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA  
 AAAGATTTTTTTTTGCGAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAATA  
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTT  
 CTTACATAAAAAATATCAGAAATACATTTTATAACTGCAGTGGTATAAATGCAAAATATACT  
 ATTGTTACATGTGAAAAAATTTTATTGACTTAAAGTTTTATTATTGTTTTTTTCTCCT  
 GATTTTAAGACAATAAGATGTTTTCATGGGCCCCTAAAGTATCATGAGCCTTTGGCACTGC  
 GCCTGCCAAGCCTAGTGGAGAGTCAACCCTGAGACCAGGTGTTAATCAAGCAAGCTGTAT  
 ATCAAAATTTTGGCAGAAAACAAAATATGTCATATATCTTTTTTAAAAAAGTATTCA  
 TTGAAGCAAGCAAAATGAAGCATATTTTACTGATTTTTTAAATTTGGTGTCTTAGATATATTT  
 GACTACACTGTATTGAAGCAATAGAGGAGGCACAACTCCAGACCCTAATGGAACACAT  
 TTTTCTCACTTAGCTTCTGTGGGCATGTGTAATTGTATTCTCTGCGGTTTTAATCTCACAG  
 TACTTTATTTCTGTCTTCTCCTCAATAATATCAAAACAATATTCAGTCACTTTTAAATGGC  
 TGCATAAATACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA  
 TTGAATGAATGAACGAAAAAAAAAAAAAAAA

**FIGURE 16**

MEPPGRRRGRAPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
 VVCSSLELAQVLPPDTLPNRTVTLLISNNKISELKNGSFSGLSLLERLDRNNLISSIDPGA  
 FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQT  
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELEPSFYMTF  
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT  
 ISNIQAGSTGNWGCCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLGIT  
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNL  
 TNAVATARQLLAYTVEANFSDKMDVIFVAEMIEKFGRETKEEKSKELGDMVDIASNIMLA  
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGTGMTCT  
 VFQKVAASDRITGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
 433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
 384-390, 403-409, 554-560



**FIGURE 17**

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAA  
TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTTGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGAGAGACGCTCCTGATCGTCGAATCC

**FIGURE 18**

MSRSSKVVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

18/249  
MSRSSKVVVLGLSVLLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS  
Signal peptide:  
amino acids 1-21

**FIGURE 19**

CTGTGCTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTT  
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC  
 GCTGCC**ATG**CCAGTGACGGTAACCCGCACCACCATCACAAACCACCACGAGCTCATCTTCGGG  
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCCTGGGTCTCCTTCGC  
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC  
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTGCTTCTCCGTGACCCTGATCA  
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGCGCAACTTCCCC  
 ATCACCTTCGCCTGCTATGCGGGCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC  
 CTATGTCCAGTTCCTGTCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT  
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCGGCCCGGCGAG  
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTGCGCTG  
 CATCATCTTCGCGTTTCATCAGCGACCCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG  
 GAGTGCACCAACGTGTACCCATCCCCTTCCCCAGCTTCTGTGCGGGCTGGCCTTGCTGTC  
 TGTCTCTCTATGCCACCGCCCTTGTTCTCTGGCCCCTTACCAGTTCGATGAGAAGTATG  
 GCGGCCAGCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT  
 GCCTGGGACCGCCGACTGGCTGTGGCCATCTGACGGCCATCAACCTACTGGCGTATGTGGC  
 TGACCTGGTGCACCTCTGCCACCTGGTTTTTGTCAAGGTCT**TAA**GACTCTCCCAAGAGGCTCC  
 CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
 TCCGCCTTTCTCTGTTTTCTCTTCCTGTCTCCCCTCCCTCCCACCTTTTTCTTCTTCC  
 CAATTCTTGCACTCTAACCAGTTCCTGGATGCATCTTCTTCTTCCCTTCTTCTTCTTCT  
 TTCCTTCTGTGTTGTTTGTGCCCACATCCTGTTTTTACCCCTGAGCTGTTTCTCTTTTT  
 CTTTTCTTCTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG  
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCTCCTGGGTTCAAGCGATTCTCCTCC  
 CCCAGCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCTGTTTCTCTTT  
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTTGCCTGTGCGCTTCTTATCTGCCTGT  
 TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCCCTCA  
 CCCACCTCCAAAGGTGTGAGCTCACATCCACACCCTTGACCCGTCCATGCCACAGCCCC  
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC  
 GTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTCTCT  
 CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCTTTAAATTAAAAAACATATATATATATAT  
 ATTTGGAGGTGAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCAGCCCTGGGTCCCTAGG  
 CCGGCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC  
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATCTCT  
 CTGTGGTATGAAAAAG

**FIGURE 20**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIFPFSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

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**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21

[illegible]

**FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHMDPNYCHPSTSLHLC  
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALES  
AFSSYSDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCLEDGLLGSPARLASQLLGDE  
LLLAKLPPSRESAFRSLGPLEAQDSLINSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCT  
 GGCACCTCTCTGCTCAGTGCGACATTGTACACTTAACCATCTGTTTTCTCTAATGCACGA  
 CAGATTCCCTTTCAGACAGGACAACCTGTGATATTTAGTTCTCTGATTGTAAATACCTCCTAAG  
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  
 TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCTTTAAAAAAAACCAATACCAAAG  
 AAGCCTACAAATGTGCGCTTAGCCAAAATTCTGTTGATTTCACGTTGTTTTATTCACTTCT  
 ATCGGGGAGCCATGGAAAAAGAAATCAAGACATAAACACAAACACAGAACATTGCAGAAATTT  
 TAAAAACAATGGAAAATAAACCTATTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA  
 GAAAAATAAACACCTCAAATCTCAAGGCGAGTCATCCCTCCTTTGAATCTACCCAACAA  
 CAGCCACGGAATAACAGATTTCTCCAGTAACATCAGCAGAGCATTCCTTTGGGCGAGCTAA  
 AACCACATCTACCATTTCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT  
 TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
 TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCTGATA  
 ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCCCTTG  
 ATAGTGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA  
 TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTACCAATAATTCAAACCTCTTCCAA  
 ATACGTGAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTTCGGGGCCATTTTAGGT  
 GCTATTCTGGGTGTCTCATTGCTTACTCTTTGTTGGGCTACTTGTGTGTGAAAAAGGAAAAAC  
 GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA  
 ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT  
 GATTACAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC  
 TCCACTTCGTACTTCTGTATTAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCTACTA  
 CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT  
 TTTGTCAAGGAGAATCATAAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
 CCAAAGGTTTTCTTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT  
 TGTATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT  
 TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCCACCAAAAAATTTCTAAA  
 ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
 TTTCTTAAATGAAAATTGAAAGGGTGCTTTTAAAGAAAATTTGACTTAAAGCTAAAAGAG  
 GACATAGCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
 TAGTACGTTATAATTTCTAGATCAGCACACATGATCAGCCCCTGAGTTATGAAGCTGA  
 CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT  
 TCTTTAAAGTCTTCAAAGTTTTGGGAATTTAACTTGTCTTAATATATCTTAGGCTTCAA  
 TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

**FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI  
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSEFVSKVPWNA  
PIADEDLLPISAHNPATPALSSNFNTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE  
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNPNTSDPQKENRNTGIVFGAILGAIL  
GVSLTLVLGYLLCGKRKTDSEFSHRRLYDDRNEPVLRLDNAPEPYDVSEFGNSSYYNPTLNDSA  
MPESEENARDGIPMDDIPPLRTSV

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311

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**FIGURE 25**

AACAGGATCTCCTCTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCGAAGATTCACT**ATG**GTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG  
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTAGGCCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
 TCATGCCCAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTATTCTGAGGATCCTGCA  
 AATTCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCGAGTTTCTCTGATAGTGACCCTGCAG  
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGCTGGGGAACGTC  
 TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG  
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG  
 TGGAGGAAATTTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
 AAGTCCTTCGCCTTCGTGCGAGAGACCTCTGCTGGGTTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**  
**AA**GAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
 CATTAAAGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT  
 AAAAAAGGAAAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAA  
 TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTTCTTTCATTTATAG  
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC  
 GTTGTTTTTTTTGTTTGTGTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG  
 GTGGAGCAATTTAAATTTGAAATATTTAAATGTTTTTGAACTTTTTGTGTAATAATATA  
 TCAGATCTCAACATTGTTGGTTTCTTTGTTTTTCATTTTGTACAACCTTCTTGAATTTAGA  
 AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
 TTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG  
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 CCTATAATAAATTTTACTCTATACAAAAA

**FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

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IIDVPVPSFSDSDPAIIHDFEKGMTAYLDLLLGNCYLPLNTSIVMPKNLVELFGKLAGS  
RYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNRKSFRLRRRDLLLGFNKRAIDKCWKIR  
HFPNEFIVETKICQE

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT  
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTGCGCGGGAGCACCAGTCCTGTACGCC  
 AAGGAAGTGGTCTGGGGGCACC**ATG**GTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG  
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCGCTCTGTGCCCTGAAGGCCACGTT  
 CCTGGAGGATGTGGCGGGTAGTGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC  
 CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGGG  
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTATCGTCTGTGCCGCGGTCA  
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC  
 GTGGACCAGAGTGACCGGGCGGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG  
 CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA  
 GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTGG  
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCAG  
 GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCCCTGTGCTTGACAGAGTGTCCACCCAG  
 TGTCT**TAA**CAGTCTCTCCCGGCTGCCAGCCCTGACTGTGCGGGCCCCAAGTGGTACCTCCCC  
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG  
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
 GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC  
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCAGTGTCCCTGTGACAGCCAGGATAAAACATCC  
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCAAACTACTTTTAAACA  
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTAATTTTCTGAAGG  
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC  
 TCAAGCGCTCTCAAAGCACCCTGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
 GATCAGGTTGAATGAATGGAATCTTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
 GCTGTGTTTGAAGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG  
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG  
 TGTCCACAATATTCGTAGTCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT  
 CTGGCAGGAGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
 CCAGGTGCTGAGATATAATGCACCAGCACAATAAACCTTTATTCGGCCTGAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852  
><subunit 1 of 1, 283 aa, 1 stop  
><MW: 29191, pI: 4.52, NX(S/T): 0  
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL  
SPTSMGPQPTTLGGPSPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA  
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP  
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE  
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

### FIGURE 29

[illegible]

**FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEG VGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSGQGLGGQGGNPGGLGTPVWHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESGIQGFRRQGVSSNMREISKEGNRLL
GGSGDNYRQGSSSWGSGGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
 383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

**FIGURE 31**

GACCGGTCCCTCCGGTCTCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGGCGGTGCTCACCG  
 TGCCCTGGCTGGTGAGTTTCTCTCCTTTGCTGACCATGTGTCTCCCTTGCTGGAATATTACCGGGACATCTCA  
 CTCTCCTGCTGCGCTGCACCGGAGCTTGGTGTGTGCGCAGGAGAGTGAGGGAGAGTGTGTTTCTGAAACAAGC  
 TGCTGCTACTTGTCTCTCTGGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACTTGTCTTTCTGGAAGAGG  
 GTCCCTCATATGCCTTTGAGGTGGACACAGTACGCCACAGCATGGCTTGACCAATCGCCTGTGGCTGGACCGAG  
 AGCTGCTTACACCTGCTGCCCTACATCGGAGAGCTCCGGAACCTGCTCGCTTCGTGGGTGTGAGGCAGTAGTG  
 GACGGAGTGGGGCTTCATGAGGAAATCACCCCCACCTACCACCAGCTGGGAGCCAGCCTTCCAGACCA  
 GCCAGGGGCTGCAGGCACAGCTCGCCCCAGGCTTTTCCACAACCAGCGCCCTCCTTGCGCCGGACCGTAGAGT  
 TCGTGGCAGAAAGAAATGGATCAAACTGTGTCAAAATATCAAGGCTACACTGGTGGCAGATCTGGTGCGCCAGG  
 CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAGGGGAGACCCAGCCAGCTGTGGAGATCT  
 TGTGTTCCAGCTGTGCCCTCAGCGGGCCAGGCATTGGCCCTGGGGCGGGAGTCTGTCAAAGGAAGAGCCCTG  
 GGGCTGTGGGGCGTGTCTCCAGAGAGAACCCGCGCAGCCGTCTGAGCAGTGCAGAGAATATGCTGTGGGG  
 TTGCAACAGAGAAAGCCTGTGCTTGGCTTCAGCCAAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG  
 TGAGTCCGACACTTCGAGGCCAGGGTCCGTAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCC**TGAC**  
 GTGCTCTCCTTTGGCCGTGGGGCCACGGGACCTTGACGAGGGAGTCTCCCCAGCACTCTGGAACAGCTCCTAGGC  
 CAGTGGGCCAGACGCTGCGGTGCGGCCAGTTCTCTGTGCCACCTGCTGAGCAGCATCTGGCAAGTGTCTGTG  
 GAGTTAGCTTCCCTCCTGCTTGCAGATCAAAATCTTATCCTAGGGCCCCCGGCACAGTACAGGCTGGAGAGAGG  
 CAGGCTCGAAGGCTTCTGCACATGCTGCTTTTCTGTGGAAGGAAGACTTCAGGGGCGGGTCCGCTGCAGCTG  
 CTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGAGTGGGACTGTGCTGCTATTCTTGCTA  
 CGGGAGCTGTTGGAGAAGGGTCTGATGGACGGATGGAGATAGAGGCTGCTGGGAGCCTCCACAGGCCCAG  
 TGGCCAGGGGACTTGTCTGAAGAAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCACTGCCAGAACCC  
 CATTTAGAGAGCTGTGATTTGGTGACGCCAAACCCGGGGCACTGTGCTGGCCACAGCTAGGGCTGAGAAGTGGCC  
 CTGCCCTTGGGCATTGCACCAGAACCTTGGACCCCCGCTCACGAGGAGGCCCAAGTGCCCAATGCAGACCTCAC  
 TGGTGGGGTGTAGCTGGGTCTACAGTACAGACTCCTGCTCTAAGGGTGTCACTGCCTGGCATCCCACCACGCGA  
 ATCCTAGAGGAAGGAGAGTTGGCCTGATTTGGGATTATGGCAGAAAGTCCAGAGATGCCAGTCTCTGGAGTAGAA  
 GAGTGGTGTGTTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTTGTCAACACAGAATTCAAGCCT  
 CATTTGCTATCCCAAGCATCTCTTAAACCTTTGTAGTCTTGGAAATCATGACAGAGGCAATGACTCCTGCTTAAC  
 TTATGAAGAAAGTTAAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT  
 ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCCTGTAATCCCAGCACTTTGAGAGGCTGAGGTGGCG  
 GACTGCCCTGAGGTGAGGAATTAAGACACGCTGGCCAAACATGGCAAAACCCATCTCTACTAAAAATAAAAAA  
 TTATTAGCTGGGCATGGTGGTGTGTGCCTGTAATCCCAGCTACTCAGGAGGATGAGGCAGGAGACTGCTTGAAC  
 CTGGAGGTGGAGGTTGCAGTGAGCGAGGTGCGACCACTGCACTCCAATCTGGGTAACAGAGCGAGACTTTCTAG  
 AAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCTGTACCTTCAGCCCTG  
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCACTTTAGAGCTTTTLAGAATAAA  
 CTGGTTTTCTTTAAAAAAGGGCGCCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT  
 TTTTCTTTTCTTTTCTTTTAAAAAGGGCTTTTATTTAAATTTCTCCCAACACGATGGCTCCTGCAATCTGCCACAGCTC  
 TGGGGCGTGTCTGTAGGGAAGAGCCCTGTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCCGCGGAGCTG  
 GCCGTGCTTGGCGCCCTGGCGTGTGTCTAGCTGCTTCTTCCCGGGCACAGAGCTGCGGGGTCTGGGGGCACCGGG  
 AGCTAAGAGCAGGCTCTGCTGCAGGGGTGGAGCCTGTCTTAACCGACACCTGAGGTGCTCCTGAGATGCTG  
 GGTCCACCTGAGTGGCAGGGGAGCAGCTGTGGCCGGTGTCTTCTYTAGGGCACTCTGGGGAAACTAAGCT  
 GGGCCCTTCTTTGCAAGACCGAGGATGGGTGGGTGTGGGGGACTCATGGGGAATGGCCTGAGGAGCTACGTGT  
 GAAGAGGGCGCCGTTTGTGGCTGCAGGGCCTGGAGCGCCTCTCTCTGAGCCTCAGTTTCCCTTTCCGTCTA  
 ATGAAGAACTGCCCTCTCGGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTTGGACGAGCGTCTA  
 GTTATTTTCACACTGTCTGCGACGTTGGCTGGGCACGTCATGGAATGGCCACTCCTCTCTGCTGCGTGGAC  
 GTCGCGTCTGGGAGTGCAGCCAGAGCGGGGCCAGAGCTGCGCTTGGGGTGGGGGAGGCGCCCGGGAGGG  
 CCTCACAGGAAGTTGGGCTCCCGCACACAGGAGCGGGCGGGCTCCCGCCGCGCGCCGCCACACCGTCCAGG  
 GGCCGCTAGACAAAGTGAAGTCCGCGTTGGGCTCGCTGCGCAGCAGGTAGCCCTTGATGCAGTGCAGCGCGCG  
 TCGTCCGCCAGCTGGAAGCAGCGCCCTCCACAGCACGAACGCCGTGCGCCT

**FIGURE 32**

MCFLNKLALLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
SLRRTVEFVAERIGSNVCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL  
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282



**FIGURE 33**

TCCCTTGACAGGCTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG  
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCTGCAGCTTCCCTTGAGGTGTGAACCCACATCCC  
 TGGCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG  
 AGTAGCAACAAAGAGCAGCGGTGACGAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT  
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGTCCCTGCGGGGCCGTG  
 GCGGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
 AACAAAGACACTGCCCTCTCGGTGCCACAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCT  
 GGGCACCAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCTGTGGCCCATTC  
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT  
 CATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC  
 AGCGAGCGGGCCTGGTGTTCGCCAACATGAAGCATATGCCGTCTCTCCCGCGCATGCGG  
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT  
 GAGCACAGGCTGGTTTACCATGGTGTATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG  
 GCATGGTCCCCCCTACTGACGCGGCGGGCCCGCTCCAGCGCATGCCCTACCACTAC  
 TACGAGCCCAAGGGGCCGAGCAATGTGTACCTACATCCAGAATGAGCACAGTCTGCAAGGG  
 CAACCACACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCTGTGGGGCCAGCTGTATGGCA  
 TCACCTTCTCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG  
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG  
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
 TGGGGAATCTGTTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC  
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTTCTGAGTCAATCTG  
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGTTTCAGAGCCCCAGGAATGGACCCCCA  
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTTGGTGTG  
 CCCCCCAATTTCCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC  
 GGCCAGAGAATTTGTGGGGTTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGA  
 GGCTGGCATCCAGGCTCTGGCTCTGCCCTGAGACCTTGGACAAACCTTCCCCCTCTCTGGG  
 CACCTTCTGCCCCACACAGTTTCCAGTGCGGAGTCTGAGACCTTTCCACCTCCCCACAA  
 GTGCCCTCGGGTCTGTCTCTCCCGTCTGGACCTCCAGCCACTATCCCTTGCTGGAAGGCT  
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTTAGGGTATTTTTC  
 GCAAACCTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTCT  
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTCTGCCCT  
 CTAGCAGGGAGGTTTCCAACCTGTGTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA  
 CTGGGGGCTTCCGAGGCTCTCCCTCGACCCTCTGTCTCTGGGATGGCTGTCTGGGAGCTGT  
 ATCACCTGGGTTCTGTCCCTGGCTCTGTATCAGGCACTTTATTAAGCTGGGCTCAGTGG  
 GGTGTGTTGTCTCTGTCTCTGTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
 GGTGGAGGGACAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG  
 GGGCGGTGACTGCCCCAGACTTGGTTTGTAAATGATTGTACAGGAATAAACACACCTACGC  
 TCCGGAAAAA

**FIGURE 34**

MSSNKEQRSVAVFVILFALITILILYSSNSANEVVFHYGSLRGRSRRPVLKKWSITDGYVPIL  
GNKTLPSRCHQCIVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH  
SSVFRVLRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQIRAGLVFPNMEAYAVSPGRM  
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRLQRMPIH  
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPST

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

**FIGURE 35**

GTTTCATAGTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACCTCAGCGGACCGGGAGCGACGAGCTT  
 GAGGGAAGCATCCCTAGCTGTTTGGCCGACAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTTGCTTGAAGGGGCTGG  
 GGCAAGAGTGAAGAGTTTTCAGAACAGCTTCTTGGAAACCATGACCCATGAAGTCTTGTGCGACATTTATACCGT  
 CTGAGGGTAGCAGCTCGAAACTGAGAAGTGGAGTGTGGCAGGGACGGCAGTATCTCTTTGTGTGACCCTTGGC  
 GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG  
 AGGCGCTGAGGTCACACTGGCTTGGCTTCCCTTCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTCCTCAG  
 GTCCCGCTCCAGCCTGGCTCCACCGTCCAGAAAGCCGAGGCACTGTGATCTTGGGCTGCGTGGTGGAAACCTTCA  
 AGGATGAATGTAACCTGGCGCTTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC  
 CACGGGACCTCTGTCATCACTGCCCTTAACAACACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCCTGGC  
 GGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAACTCCAGGACTTCAAGTTAGATGTGCAGCAGCTG  
 ATTGAAGTGGATGAGGGAACACAGCAGTCACTTGCCTGCCACCTGCGCTGAGAGCCACCCAAAGCCAGGTCGGG  
 TACAGCGTCAAAACAAGAGTGGCTGGAGGCTCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT  
 GTGAATGCCAGCCAGGAGGAGGCGATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAAGAAC  
 TCCGCTCCAGCGACAGGCTACGTGTGCGCCGTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC  
 CAAACCATCATCGTCAACAAAGCCAGAGTCTCATTTCTGGAGTGTGTGGCCAGTGAATCCACCCCCAGCGGTC  
 ACCTGGGCGAAGGATGGGTCCAGTGTCACCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTTCTCATCGAC  
 ACCACAGCGAGGAGGACTCAGGCACTACCGCTGTCATGGCCGACAATGGGTTGGTGGCAGCCGGGGCAGCGGTC  
 ATCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTCAACATGGAGCTATCCAGCTGCTCATCCCTGGGGC  
 CAGAGTGCCAGCTTACCTGTGAGGTGCGTGGGGAACCCCGGCTCCGCTGCTGTGCTGAGGAATGCTGTGCTCC  
 CTCATCTCCAGCCAGCGCTCCGGCTTCCCGCAGGGCCGTGCGCGTGTCTCAGATGGGCTCTGAGGACGAAGG  
 GTCTACCACTGTCATGGCCGAGAACAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTCGGCACTCCAGGCCAAGC  
 ATAAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATACCTCTTCAAACTTCGGCAAC  
 CCTGAGCAGATGCTGAGGGGGCAGCCGCGCTCCCCAGACCCCAACGTCAGTGGGGCTGCTTCCCCGAAGTGT  
 CCAGAGAGAAGAGCGGAGGGGCTCCCGCAGGCTCCCATCATCTCAGCTCCCGCGACCTCCAGACAGAC  
 TCATATGAATGGTGTGGCGGCTCGGCATGAGGGCAGTGGCGGGCGCCAACTCTCTACTATGTGGTGAAGAAC  
 CGAACGAGGTCAAAATTCCTCTGACGATTGGACCATCTCTGGCATTCAGCAACACGACCGCCCTGACCTC  
 ACCAGCTGACCCCGGAGCTTGTATGAAGTGGAGTGGCAGCTTACAACCTGTGGCGGAGAGGGCCAGAGACC  
 ATGGTCACCTTCCGAACCTGGACGCGCGCCCAACCCAGAGTCAATGGCCAGCAAGAGCAGAGTCCAGAGAGC  
 GACCTTGAGGCGAGTCCCAGAGCAGCAGCCAGCCAGACCGGCGGCTTCCCCCCAGAAGTCCCCAGAGC  
 CCCACCATCTCCAGGCGCTCCGAGAAGCTCAGTGTACGTGACCTGGATTCCCGTGGGAATGGTGGGTTCCCAATC  
 CAGTCTCTCGTGTGGAGTACAAGACTAAGAAAGTGGGAGACTGGATTCTGGCCAGCCAGCGGCATCCCCCA  
 TCGCGGCTGCTCGTGCAGTACCGGCGCTAAGAGAAAGGCACCTCTACAAGTTCTGACCTCGGGCTCTGAACATG  
 CTGGGGGAGGCGGACCCAGCGCCCTCTCGGCCCTACGTGCTGTGCGGCTACAGCGGTGCGGCTACAGAGG  
 CCGCTGGCAGGTCTTATATACCTTACCGGATGCGGCTCAATGAGACCACTCATGCTCAAGTGGATGATCATC  
 CCAGCAAGTAAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGAACATGATAGT  
 GACTACAAGAAGGATATGGTGAAGGGGACAGTACTGGCACTCCATCAGCCCACTGCGAGCGAGACCTCTCAG  
 GACATTAAGATGCAGTGTCTCAATGAAGAGGGGAGAGCGAGTTACAGCAACGTGATGATCTGTGAAGCAAGCT  
 CGGAAGTCTTCTGGCCAGCCTGCTCGACTGCCACCCCAACTCTGGCCCCACCAAGCGCGCCCTTCTGAAAC  
 ATAGAGCGGCGGTGGGCACTGGGGCCATGGTGGCTCGTCCAGCGACCTCCCTATCTGATTGTGCGGGGTGCTC  
 CTGGGCTCCATCGTTCTCATCATCGTCACCTTATCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAAACAT  
 ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCCACCCTCTGCCGATATACTATGGTGCCATTGGGAGGACTC  
 CCAGGCCACAGGCGCAGTGGGACGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG  
 AATAGGGGCTGCCCTCGGCTCGAGTGGGCTACCCGGGCTGAAGCCCGAGCAGCAGTCCCGAGGCGAGCTTCAG  
 CAGCAGAGTGACACCAGCAGCTGCTGAGGACAGCCCATCTTGGCAATGGATATGACCCCAAGTCAACAGATC  
 ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTCTTTCTTATACACACTGCCCGACACTCCACTCACCAGCTG  
 CTCAGCCCCATCGACTGCTGCCAAGCGCAGGAGCAGCTGCTGCTGTGGGCGAGTCAGGGGTGAGGAGAGCC  
 CCCAGTCTCTGTCTGGAAGCAGTGTGGGACCTTCCATTCTACTCAGGCGCCCATGGTGTGCTTGGGCTTTGTG  
 CCAGTTGAAGAGGTGGACAGTCTGACTCTGCCAAGTGAAGTGGAGAGACTGGTGTCCCAGCACCCTGAGG  
 GCTACGTAGGACAGCAACTGGAACTGACGCTTCCCCGGGCACTGGTGGTGTGCTTTTGAACACCACT  
 CTCACAATTAGGCAGAAGCTGATATCCAGAAAGACTATATATGTTTTTTTTTAAAAAAAAGAAAGAAAA  
 AGAGACAGAGAAAATGGTATTTATTTTCTATTATAGCCATTTATATATTTATGCACTTGTAATAAATGTA  
 TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCGTGAAGTTGGAGGGGAAAAATAAGAAAGCTGCCA  
 CCTAACAGGAGTCAACCCAGGAAAGCAGCGCAGGCTGGCGCGGGGACAGACTCTCAACTGGGGCTCTCGAGT  
 CGAGCGAGGCTGCAGGAGGGCCACAGATAAGCTGGCAAGAGGAGGATCCAGGACCATGGTTCATCAGAGCA  
 TGAGGGAACAGCAAGGGGACCGGTATACAGGCTGGAGACACCCACAGATGGCTGGATCCGTTGCTACGGGAA  
 ACATTTTCTAAGATGCCATGAGAACAGCAAGATGTGTACAGCACTATGACAGTAAAAAACCTTCCAGAAAT  
 CAATATCCGTGGCAACATATCTGTGAAAACAAACACTGTAACCTCTAATAATAATGTTAGTCTTCCCTGTAAAA

**FIGURE 36**

MLRGTMTAWRGM RPEVTLACLLLATAGCFADLNEVPQVTVQ PASTVQKPGGT VILGCVVEPP  
 RMNV TWR LNKELNGSDDALGV LITHGTLVIT ALNNHTVGRYQC VARMPAGAVASVPATVTL  
 ANLQDFKLDVQH VIEVDEGNTAVIACHLPESH PKAQVRYSVKQEWLEASRGNYLIMPSGNLQ  
 IVNASQEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSL  
 ILECVASGIPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS  
 RRALRVLSMGPEDEGVYQCAENEVGS AHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEKGQGAPEAPIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGR LSPPEAPDRPTISTASE  
 TSVYVTWIPRNGGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV  
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMI PASNNNT  
 PIHGFYIYRPTDSDNDSDYK KDMVEGD KYWHSISHLQ PETS YDIKMQC FNEGGESEFSNVM  
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSI VL  
 IIVTFIPFCLWRAW SKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK  
 SSPDEGSFLYTL PDDSTHQLLQPHHCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHS G  
 PPCC LGLVPVEEVDSPDSCQVSGGDWCPQHVPV GAYVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

**FIGURE 37**

CGGGAGGCTGGGTGCTCATGATCCGGACCCATTGTGCGCCTCTGCCCATCGCCTGCTCCTC  
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCACGGGCGCGAGGGTCCCCGCGC  
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC  
 AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
 CACCCCCAAAACCTTGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG  
 TGGACGGCCACAATGACCTGCCCCAGGTCTTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCAGGACCAGACTGCCGTGCGCC  
 TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCTCCTACTCTGAACTCGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTTCAGACAC  
 CACATGTACACCAACGTCAGCGGATTGACAAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTTG  
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT  
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGAAAATTATGACGGGACT  
 GGCCGGTTCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCGTGAAACCTGCTGCGGGTCT  
 TCAGACAAGTGGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGACCCCGTGAGGCTGAGTTT  
 CCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCCTCAGAATGGACACCAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCCT  
 CCCCATACCTTGTTCCAGGCCTTGTTGGGTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC  
 TGCT**TGA**CACAGTCGGTCCCCGCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
 AGTTTATTCACAAGCATATGCTGAGAATAAACAATGTTACACATGGAAAA

**FIGURE 38**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRYLRRLLLLLLLLLLLLRQPVTTRAETTPGAPRALSTLGSPSLFTTPGVPS  
 ALTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ  
 TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS  
 QKLACLIQVXGGHSLDSSLSVLSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT  
 SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL  
 LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDV  
 STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYGQLSTSCH  
 SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGCATG  
 AAGCTCTTATCTTTGGTGGCTGTGGTTCGGGTGTTTGTGGTGCCCCAGCTGAAGCCAACAA  
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
 GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCACCATCAAGGTCATCATTGTCTATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
 ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCACAAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC  
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTAGATGGGCTGG  
 TGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTCCTCCTT  
 CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT  
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGGAAGGCAGGCCAGAAGGGA  
 ATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG  
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCTTGGAAGATAAAGCTGGGTCTTCA  
 GGAAGTCAAGTGTCTGGGAGGAAAGCATGGCCCAGCATTGAGCATGTGTTCTTTCTGCAGTG  
 GTTCTTATCACACCTCCCTCCCAGCCCCGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCACTGGGTCTTCAGGGTGCAGTGGA  
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT  
 CTGCTGCCGGTCCCCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC  
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
 CACCACAGCCCCGTGTAAGTGGGTGCTCTGTCCCTGAACTTCGTTGTACAGTGCATGGA  
 GAGAAAATTTGTCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTTG  
 TTTATTTCTCTCA

**FIGURE 40**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM

PVPGHDVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE

QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50



**FIGURE 41**

AGCGGGTCTCGCTTGGGTTCCGCTAATTCTGTCTGAGGCGTGAGACTGAGTTTCATAGGGTCCTGGTCCCCGA  
 ACCAGGAAGGGTTGAGGGAACAATCTGCAAGCCCCCGCAGCCCAAGTGAGGGGCCCTGTGGGGTCTCTCC  
 TCCCTTTTGCATTCCACCCCTCCGGGCTTTGGCTCTTCTCGGGGACCCCTCGCCGGGAGATGGCCCGGTTGATG  
 CGGAGCAAGGATTCGTCTGTCTGCTGCTCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT  
 TCGCGGGCAAACTCAACTCCATCAAGTCTCTCTGGCGGGGAGAGCCCTGGTCAGGCCGCCAATCGATCTGCG  
 GGCATGTACCAAGGACTGGCATTTCGGCGGCAGTAAGAAGGGCAAAACCTGGGGCAGGCCCTACCCCTGTAGCAGT  
 GATAAGGAGTGTGAAGTTGGAGGTTATGCCACAGTCCCAACCAAGGATCATCGGCTGCGATGGTGTGTCGGAGA  
 AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCGGTACCCGCTGCAATAATGGCATCTGTATCCAGTT  
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACACGGTCATTAC  
 TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA  
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA  
 CCAGTGTCTCCATCAGGGGGAAGTCTGTACCAACACGCAAGAAGGGTTCTCATGGCTGGAAATTTCCAGCGT  
 TGGCACTGTGCCAAGGGCTGTCTTGCAAGATATGAAAGATGCCACCTACTCTCCAAAGCCAGACTCCATGTG  
 TGTGAGAAAATTTCATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG  
 CATGGTGGAAAATAAGGTTGAGATGCAGAAGAAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCAAA  
 AAAGGGGAGAGAAAACATGACTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCCTATTATG  
 CAACCTGTCTATGTAATAATGTACACATTTTGGAAAATGCTATTATTAAAGAACAAAGCACACAGTGGAAAT  
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC  
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGAATAACTTGTTA  
 TCAATAGGTTCTAAAATAAAATTTGCTAAACAAGAAATGAAAACATGGAGCATTTGTTAATTTACACAGAAAAT  
 TACCTTTTGATTTGTAACACTACTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT  
 TTCCAAATAAATGCAAAATAATGGCCAGTTGTTAGGAAGGCCCTTAGGAAGACAAATAAATAACAAACAAACAG  
 CCACAAATACTTTTTTTCAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAACAGTTCC  
 TTCAGATTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTTCCA  
 AACTATACCCATAAATTTGACTAGTAAAATACTTACACAGAGCAGAATTTTCACAGATGGCAAAAAAATTTAA  
 GATGTCCTCAATATATGTGGGAAAGAGCTAACAGAGAGATCATTTATTTCTTAAAGATTGGCCATAACCTATATTT  
 GATAGAATTAGATTGGTAAATACATGTATTATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG  
 CACTGGAGTAAGCAAGAAAATTTGGAAAACCTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATGCTG  
 AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT  
 CATAATATTACTATGCAGATGAATTGAGTGTGAGGTCCTGTGTCCTACTATCCTCAAATATTTATTTTATAG  
 TGCTGAGATCCTCAATAATCTCAATTTGAGGAGTTTACAAAATGTACTCTGGAAGTAGACAGAGTAGTGAGG  
 TTTCAATGGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAAATTTCTTCCAAACCTCTGCAGCATCTG  
 CTTTATTGCCAAGGGCTAGTTTCGGTTTTCTGCAGCCATTCGGGTTAAAAAATATAAGTAGGATAACTTGTA  
 AACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTGAACCACTTTACTACTTTTTTTAAACTT  
 AACTCAGTTCTAAATACCTTTGCTCGGAGCACAAAACAAATAAAGGTTATCTTATAGTCGTGACTTTAACTTTT  
 TAGACCACAATTCACTTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCCAGTAG  
 AGATTGAGTTTGAGCCTGTATATCTATTAAAAATTTCAACTTCCACATATATTACTAAGATGATTAAAGACTTA  
 CATTTCTGCACAGGCTCTGCAAAAACAAAAATTTATAAATAGTCCATCCAGAACCAAGTTTGTATAAACAGGT  
 TGCTATAAGCTTGTGAATGAAAATGGAACATTTCAATCAACATTTCCATATATAACAATTTATATATTTTACAAT  
 TTGGTTTCTGCAATATTTTCTATGTCACCCCTTTTAAAAATTTATTTTGAAGTAATTTATTTACAGGAAATG  
 TTAATGAGATGATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATTTTGAGCTATTGAC  
 TTTGTAAATTTAGGAAAATGTATAAAGATAAAATCTATAAATTTTCTCTCTAAAAACTGAAAAAATAA  
 AAAAAAATAAATAAATAA

**FIGURE 42**

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCRDRGMCCPSTRCNN  
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

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**FIGURE 43**

TCTCAATCTGCTGACCTCGTGATCCGCTGACCTTGTAAATCCACCTACCTTGGCCTCCCAA  
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCGCAACATCACGTTTTTAAAAATTGATT  
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTGAGAATGAGGAAGGA  
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAAATCTTG  
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTGTTCCTTTTATCCCCCT  
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA  
 TCACCAGCTCCCAGATTTTGGACCAAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAATACTACTTCTTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
 CAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACGTGTTCTCTCT  
 CCTGGTTTTGGAGTCCTTTCCCTTCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG  
 TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG  
 ATCCCAGCTTCTGCAGTGGAAATGCCTGGTTCAGCAGATGTACAGGATTAAATGTGCAGTT  
 TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
 AAAATAGTAATCAGATTTCCCATCAGCTTGTATTCTGAAGCTTTAAGTGAGCCTTTGAATACA  
 TCTTTATCAATGACCAGTGACGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC  
 AGAGTTCTGTGCATAACAGGATCCCATAACAAAGCCCTGTGAGTTTATCAGAGTCAGCTCCA  
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTTGTCTATGGCTGGTGCCAACCAAACAGAGGAAGAGGATAGCTCACGTGA  
 TGTGGAAACACCAAGTTGGTCAATGGCTCATTCTGTTAAAGCAGGCCCTTTTGCTTTTTTGT  
 TTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
 GGTGGTCTCATATTTCTGCCCATAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT  
 TTTAAAGATGCTTGGGCCAGGCGGGTGGCTGATGCCCATAAATCCAGTGCTTTGGGGGGCC  
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAACTC  
 TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCTGCCTGTAATCCCAG  
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
 GTCTGAAAAGA

**FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
PSTQQNSTSHPTTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP  
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK  
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP  
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPKQQRKRIAHVMWKT PVGQWLIR

**Signal peptide:**

amino acids 1-24



**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT  
 TTGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCTTGGAGGTACCGACGGCCCCCGGCCACCCCCGCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGCACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCGGG  
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA  
 CGGGCCCCCTTTTCTGCGCGACCGCTGGGTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCGCTTTCACCTGACGGTCGCCGAACCCACGC  
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCACG  
 ACCCCACACTGGCGCGGGCCACAACGTCAATGTCATCGTCCCCGAGAGCCGAGCCAC  
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC  
 TGTCTCTGGCGCCCGCAGGCGCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGTTCCGGAAGGAGAAT  
 GCAAA**TAG**GAGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTCCAGCGGCTGGTCCCGCTTTCTT  
 GGAATTTGGCCTGGGCGTATGCAGAGGCGCCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAACC  
 AAAATCCCACTGATGCCATCATGCCCTCAGACCCCTTCTGGGCTCTGCCCGTGGGGGCTG  
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACCTGGGGTCAGCCTCA  
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA  
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT  
 CCTCCTGGGGTGTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTGCTCCTCTGTGTTG  
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCCATCCCTACCTAGCCTTG  
 CTCTAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCTT  
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGACCCACATTT  
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCATCTGATTTTTAAAAAAAAA  
 AAAAA

**FIGURE 46**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWD RQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDL DKGFRKENCK

```

**Important features:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGCGGCGTGGCGCAGCGGCGAC**ATG**GCCGTTGTCTCAGAGGACGACTTT  
 CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
 ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT  
 GTGGCACATACATCATCTTCTTACGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTCTTT  
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
 GGACCTTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
 TGCCCTCCATGCTGTGCTGGTGGCCAACTTCTGCTGTCAACAGGGTTGCAGTCCACATC  
 CGTGTCTTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCAGTGGTGAA  
 GGTGGACACTTCCCTCGGACCCGTGGTTTTTTTCGGGTACCATTTGTCTGCATGGTGATCC  
 TCAGCGTGCCTCCACTGTCTTACGAGCAGCATCTACGGCATGACCGGCTCCTTCCCTATG  
 AGGAACCCCCAAGCATGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC  
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG  
 CCACCATCTTCTCTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
 AGGTACTACATGAGGCTGTTCTTGGCGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCA  
 GGACTCCCTCAGTGCCCTTTCGGTGGCCTCCAGATTATTGATTCCACACACCCCCCTCTCC  
 GCCCCATCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATACC  
 AGCCTCATCTACCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
 GTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACCTTGTGACCTAT  
 GTGGCCGGCAGCTACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCCTCCCAGGG  
 TTCGTGCTCCTCCGACCTGCCCTATCCCCCTCTTCGTGCTCTGTAACCTACCAGCCCCGCT  
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCGCACTCCTCAGCTCCCTGCTGG  
 GGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGGCCTAAGATTGTGCCAGG  
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG  
 CTCAGCCTGCTCTACCTCCTGGTGCACCTCATC**TAGA**AGGGAGGACACAAGGACATTGGTG  
 CTTAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC  
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA  
 GTGAGCCACGTCCATGCCATTCGGTGCAAGGCAGATATTCCAGTCATATTAACAGAACCT  
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA  
 ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCCGCTTAGAGTTATTACA  
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTGTCAACCTCCCAGCTGCGCTCATTCCAGCT  
 GACAGCAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGTCTCCCTGGAATGGA  
 AGTCCCCTGGCATGGTCAGTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
 GCGGGTGAACAACCTGCCACTAACCAGACTGGAAAACCCAGAAAGATGGGCCCTCCATGAAT  
 GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
 TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC  
 TTTCAAGTGTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
 GTATTCAAAAA

**FIGURE 48**

MAVVS EDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPGLQRPEDRFCGTYYIFFSLGI  
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
 LVNRVAVHIRVLASLTIVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVNRNSALAFFLTATIFLVLCMGly  
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF  
 CVTYVFFITSLIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
 305-330, 448-472



**FIGURE 49**

GACAGTGGAGGGCAGTGGAGAGGACCGCGTGTCTGTGTACCAAGAGCTGGAGACACCA  
 TCTCCCACCGAGAGTCA**ATG**GCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC  
 TCAGCCTGGTGGCCTCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC  
 ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCTT  
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC  
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC  
 AGTACGACAAGAACAGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
 AAGGTGCCCCGAGAAGCTGGGCTACGCCTTGCCTCCCCAGGAAAAGGGCCACTCGCCCGAAGA  
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG  
 CGATGAAGAAGTTTGAAGGCACACGCTCTTGGAAATATCTTCTCGGGGAGGGGAACCTGAGC  
 CGGCCGGCGCTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT  
 CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGGACCTGCTGCCGCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC  
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGCTGACGGCGAGCGGACCGG  
 CGGTGAAGCGCATCACCTTCTCGCCGCGCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG  
 CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGACGGCCCTTCTGGCGCGAGGA  
 GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC  
 CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCGGACGCGGCGGCAGCGTTCGCC  
 GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC  
 TGTCGTGCGCCAGCTCTGGGACGGCACCGGCGTCTCAAGCGTTGGGCGGAGGACCAGCACA  
 GCCAGGGTGGCTTTGTGGTACAGCCGCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG  
 GTCCCTTATGGCCGCATCTACTTTGCCGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA  
 GACGGCGGTCAAGTCGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCCTGCAT  
 CGGACACGGCCAGCCCCAGGGGCGACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG  
 GTGGCCAGCAGCCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG  
 CCAGTTATCTCTCAAAACACGACCCACACGAGGACCTCGCAT**TAA**AGTATTTTCGGAAAAA  
 AA

**FIGURE 50**

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWI GELGAMRMPSSHRIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALR  
AHSCLSDR LQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGP HDVHVQIETSPPARNL  
KVLKADVLLTASGPAVKRITFS PPLPRHMQEALRRLHYVPATKVFLSFR RPFWREEHIEGG  
HSNTDRPSRMIFYP PREGALLLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

**FIGURE 51**

CTGACATGGCCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCCTTCTGCCTGCAT  
 GGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACACGAGCGAGGGGAAGAGGACAGGGACTCGTGTGGCAGGAA  
 GAACCTCAGAGCCCGGAAGCCCCATTCTACTAGAAGCACTGAGAGATGCGGCCCCCTCGCAGGGCTCTGAATTTCT  
 GCTGCTGTTTCAAAAGATGCTTTTATCTTTAACTTTTGTCTTTCCCACTTCCGACCCCGCGGTGATCTGCAT  
 CCTGACATTTGGAGCTGCCATCTCTTGTGGCTGATCACCAGACCTCAACCCGCTTCTACCTCTTCTTCACTTGAA  
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGTTTCCAGAAAGAACAATGACCTAACAAAGTTGCTG  
 CTTCTCAGATGCCAAGCACTATGTATGAGTTTCCAAAGAGGACTCGCTGTGCTGACAATGGGCCCTGCTTGGG  
 ATATAGAAAACCAAACGACCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTC  
 CTGTCTCTTGCATAAAGGTTATAAATCATCACCAGACAGTTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTG  
 GATCATCTCCGAATTGGCTTGTACACGTAATCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAAGAAGC  
 CATCGTACATATGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCAAAAGGCATTGGTGCTGAT  
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTGTATGATGACCTGAA  
 GCAAAGAGGGGAGAAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAAGAGCACTTCA  
 AAAACCTGTGCCCTCTAGCCCAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCAAGGTGACCCCAAAGG  
 AGCCATGATAACCCATCAAAATATTGTTCAAATGCTGCTGCCCTTCTCAAATGTGTGGAGCATCTTATGAGCC  
 CACTCCTGATGATGTGGCCATATCTTACTCCCTCTGGCTCATATGTTGAGAGGATTTGACAGGCTGTTGTGTA  
 CAGCTGTGGAGCCAGAGTTGATTTCTTCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGCTTGAAGCC  
 CACATTGTTTCCCGCGTGCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCTTT  
 GAAGAAAGTTCTTGTGTAAGCTGGCTGTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG  
 TTTCTGGGACAAGCTCATCTTTCGAAGAATCCAGGACAGCCTGGGCGGAAGGGTCTGTGTAATTTGCTACTGGAGC  
 TGCCCCCATGTCCACTTCAGTCATGACATCTCTTCCGGGACGCAATGGGATGTCAAGGTGATGAAGCTTATGGTCA  
 AACAGAATGACAGGTGGCTGTACATTTACATTTACCTTGGGACTGGACATCAGTTCAGCTTGGGGTGCCCTGGC  
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACCTACTTTACAGTGAATAATGAAGGAGAGGTCTGCAT  
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCCTGAGAAGACACAGGAAGCCCTGGACAGTGATGGCTG  
 GCTTCACACAGGAGACATTGGTGCCTGGCTCCCGAATGGAACCTCGAAGATCATCGACCCGTAAGAAAGAACATTTT  
 CAAGCTGGCCCCAAGGAGATACATTGCACAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCACTGTTACA  
 AATTTTTGTACACGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGTGGTTCCTGACACAGATGTAATTCCTC  
 ATTTGCAGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAAGTGTGCCAAAACCAAGTTGTGAAGGGAAGCCATTTT  
 AGAAGACTTCAGAAAATTTGGGAAAGAAAGTGGCCTTAAACCTTTTGAACAGGTCAAAGCCATTTTCTTCTATCC  
 AGAGCCATTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAAGCAAGGAGGAGAGCTTTCAAAATACTT  
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATAGGATAGGTACTTAAGTACCTGCCGCGCCACTG  
 TGCATGCTTGTGAGAAAATGGATTAAAACTATTCTTACATTTGTTTGGCCTTCCCTCCTATTTTAAAAAGC  
 TGTTAACTCTAAAGCAATAGCTTTTGTTTATATTGAGACATATAATGTGTAACCTTAGTTCCTCAAAATAATCA  
 ATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAAGCTTCAGGGCTACTTTTATCAACATGCCTGTCTCAA  
 GATCCAGTTTATGTTCTGTGCTCTTCTCATGATTTCCAAACCTTAATACTATTAGTAACCAAGGTTCAAGGGT  
 CAAAGGGACCCCTCTGTGCCCTTCTTCTTGTGTTTGTGATAAACATACTTGCCAACAGTCTCTATGCTTATTTACA  
 TCTTCTACTGTTCAAACCTAAGAGATTTTAAATTCGAAAACCTGCTTACAATTCATGTTTCTAGCCACTCCAC  
 AAACCACTAAAAATTTAGTTTTAGCCTATCACATCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
 CTGCGTAATTTAAATTTGTGTAATGAAGGAAAGTTTGTATCATACCAACATTTCTTAACTCTCTAGTTAGATA  
 TCTGACTTGGGAGTATTAATAATTTGGGTCTATGACATACGTGCCAAAAGGAATGCTGTTCTTAAAGCATTATTTA  
 CAGTAGGAAGTGGGAGTAAATCTGTTCCCTACAGTTGCTGCTGAGCTGGAAGCTGTGGGGGAAGGAGTTGACA  
 GGTGGGCCCCAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCTGAACTGGGAACAAAGATCT  
 ACAGGCAAGCAAGATGCCACACAACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCCTTGGATT  
 AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAATTAAC  
 TATTACAGATAAAAA

**FIGURE 52**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFN  
FLFSPPLTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTS  
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYS  
PDQFVGIFAQNRPEWIISELACYTYSMAVPLYDTLGPDAIVHIVNKADIAMVICDTPQKAL  
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED  
LSVICFTSGTTGDPKGAMITHQNIVSNA AFLKCEHAYEPTPDDVAISYLP LAHMFERIVQ  
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPVPRLLNRIYDKVQNEAKTPLKKFLLKLA  
VSSKFELQKGII RHDSFWDKLIFAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY  
EAYGQTECTGGCTFTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK  
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR  
SQPVLQIFVHGESLRSSLVGVVVPD TDVLP SFAAKLG VKGSFEELCQNQVVREAILEDLQKI  
GKESGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAARGELSKYFRTQIDSLYEHIQD

**Important features:**

**Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

**FIGURE 53**

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCCGAGCGGGG  
 CCCGGGGCCCCCTAAGCCATTCTTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT  
 CCGGT**ATGG**GACGACTGGAAGCCCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG  
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA  
 GACAGGGGGCGTGCTTTTCTGCTGGTGACTGTCTATTGTCAATATCAAGTTGATCCTGGACA  
 CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC  
 CTAGGCCGCTGGAGCCCCACGGCGCAGAGGCAGTGCTGCCCGGGGTCCTGGACGTAGA  
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGATGGCACCACGGTGCTGGAGGATG  
 AGGCCCCGGGAGCAGGGCCGGGGCATCCATGTCATTGTCTCAACCAGGCCACGGGCCACGTG  
 ATGGCAAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTT  
 CAACATGGTAGCGCCCCGGCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGTGAGGAGCCTGGGAGCCAGGCTGGCCCTGCCCTGGGC  
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTTC  
 TAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCCTGTCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC  
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA  
 GTTCAGCCCTGACCCACTCCAGACAACAAGGTCTCAATGTGCTGTGGCTGTGCTTGCATTGCAG  
 GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTAGCCCCAGGGGGTGTCT  
 CCTCAGATGATAACAGTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT  
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGATGCCCGCGTGTCTCAGC  
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTCAGTTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCCTGGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC  
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCGTAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACG  
 TTTCCCGATCCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACAGAGGCC  
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAGAAGCTTATGAAGTGAAGTTACAGGCTGCTCAGTGAGGCTGAGGTCTGGACC  
 ACAGCAAGAACCCTTGTGAAGACTCTTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
 TTTATTTCGAATGGAGAAGATGATGACTTCAACACCTGGACCCAGCTTGCCAAGTGCCCTCCA  
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAAGA  
 ACCACTTCTCGGTGGTGGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCTCAGTC  
 ACCCAATTTTCTGGAGCCACCCCCAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC  
**ATGA**AGCCTCCTCCAGGACCTTGGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT  
 TCCTTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTAAACA  
 TGAGACTTAAATTACTAAGGAGGGGTTCCCTGCTCCACACCCCGTTCTGTAGTT  
 AAAAGCTTATTTATTTCTTCTTGTGGAGAAGGGCAGGAGTACCTGCGAATCATTACG  
 ATCCCTAGCAGCTCATCCTGCCCTTTGAATACCCTCACTTTCCAGGCCTGGCTCAGAATCTA  
 ACCTATTTTATTGACTGTCTGAGGGCCTTGAACAACAGGCCGAACCTGGAGGGCTGGATTTC  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC  
 CACCCATGGACAGGCCAGCTGGGGCCCATGCTGACACAGCTCACTCAGAGACCCCTTA  
 GACTGAGCCAGGCCTCCTCTCAGCCTTCTCTTGTCCAGATTTCCAAGCTGGATAAGTT  
 GGTCAATTGATAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 54**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTIVIVNIKLILDTR  
 RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA  
 REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFNLMVAPGRVLICTVKDEGSFHLK  
 DTAKALLRSLGSQLGAPALGWRDTHAFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSS  
 AEEAECHWADTELNRRRRRRFC SKVEGYGVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN  
 RPNLYRMLRSLLSAQGVSPQMITVFIDGYEPEMDVVALFGLRGIQHTPISIKNARVSQHY  
 KASLTATFNLFPFAKFAVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA  
 EDPALLYRVETMPGLGWLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS  
 RSYHFGIVGLNMNGYFHEAYFKKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLEAEVLDHS  
 KNPCEDSFLEPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVDRGNHRLWRLFRKKNH  
 FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAAGCTGGAAGCCCACTCTCTTGGAAACCACCACAC  
 CTGTTTAAAGAACCCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA  
 AAGAGGGGCAGAAATGGATGATTTTCATCTCCATTAGCCTGCTGCTCTGGCTAGTTGGTGGGATGTTA  
 CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGAAGTGTCTTGG  
 GTGCTGGCCTTCTCTGTGGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTATGAA  
 GATATTCTTGGGAAACACCACCAAGCAAGTGAACACATAATGTGATTGCATCAGACAAAAGCAGC  
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTGCATGCCATATATTGGTG  
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTGTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT  
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAAATCACCACCAGCTGGGTCTGGTTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG  
 TGTTTTTGGCAATCATGCTACATAAGGCACCAGTGTCTTTGGACTGGTTTCCTTCTTGATGCATGCT  
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGTCATTGGCAGCACCAGTTATGTCCAT  
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAGAAGCCCTTTTTCAGAGGTGAACGCCACGGGAGTGG  
 CCATGCTTTTTCTGCGGGGACATTTCTTTATGTTGCCACAGTACATCTCCTCCCTGAGGTGGGCGGA  
 ATAGGCGACAGCCACAAGCCGATGCCAGGGAGGGAGAGGCCCTCAGCCGCTTGGAAAGTGGCAGCCCT  
 GGTTCTGGGTGCTCATCCCTCTCATCCTGTGCTAGTAGGACACCAGCATTAATGTTCAAGGTCCAGC  
 CTTGGTCCAGGGCCGTTTGGCATCCAGTGAGAACAGCCGGCAGGTGACAGCTACTCACTTCCTCAGTC  
 TCTTGCTCACCTTGGCAGCTCTCTACATGTATTCTAGAGTCCAGAGGGGAGGTGAGTGTAAAACCTG  
 AGTAATGGAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT  
 TATCTTTTAAAGGCCCTTGACATTTTGGCTTTTAAATATTTCTTTAACCTTATTTCTCAGGGAAGATG  
 GAATTTAGTTTAAAGGAAAGAGGAGCACTTCATACTCACAATGAAATAGTGATTATGAAATACAGT  
 GTTCTGTAATTAAGCTATGCTCTCTTTCTTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTT  
 AACATGGTTCACCACATGTAAGACTGGTGTCTTAGCATCTATGCCACATGCGTTGATGGAAGGTGATA  
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAAATGATAGC  
 AAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAGGGATGCTAGAGGGATT  
 TAAACAGCTCCTTTGGCAGCTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG  
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAAGAT  
 ACCTGTCTCCACATTCTAGAGAGGAGCCAGTTCTAGTAGTTTCAGTTCTAGGCTTTCTTCAAGAA  
 CAGTCAGATCACAAGTGCTCTTTGGAATTAAGGGATATTAATTTTAAAGTGATTTTGGATGGTTAT  
 TGATATCTTTGTAGAGCTTTTTTAAAGACTACCAAATGATGGTGTGCTTTTTTTTTTTTTTTTTTT  
 TTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTGAGCTTT  
 GGCGCACTGTGCTTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTTGCCTA  
 TTGATTTAAAGCTTATTTGGAATCATGTCTTTGTCTCTTCGCTTTTTCTTTGCTTTTCTTTCTAACTTT  
 TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAAT  
 CTTATCAGGACAACCACTTCTCGAAGTGTAAATGAAGATAATAATATCTTTATTCTTTATCCCCTT  
 CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCCTCATGTGTAA  
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATA  
 ATTTTTTTTTCATATTTGGCAAAATTTTGTAAACCCTGCTTTGTCAAAATAGTGATAATATTGTAT  
 TATTAATTTATTTTACTTTCTATACCAATTTCAAACACATTACATAAGGGGGAACCAAGACTAGTT  
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCATG  
 ATTTATTCCTTCATGAATTTGCTCACTGGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTGTGCT  
 GGCCACAGTGAGGAAAGTAGCACAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACA  
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAATGACTTCTTTGATTGGATGTTAACAGCT  
 GACTGTGTGAGACTTGAGTTTCTCATCTAGTCTTCAAACATAATGTTGGCTAGATTCTCTCTGGA  
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

**FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIP LAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVEMLLVDQ  
IGNSHVHSTDDPEAARSSNSKITTTGLV VHAAADGVALGAAASTSQT SVQLIVFVAIMLHK  
APAAFGLVSFLMHAGLERNRIRKHL LVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIP LILSVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304



**FIGURE 57**

GCTCGAGGCCGGCGGCGGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC  
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG  
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC  
 ATCGTCTTGCGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGACCTCCAGACACGGAT  
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA  
 AGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA  
 TAACATCACACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA  
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG  
 AGGAAGTTCTCCTACGACCTGAGCCAGTGATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
 GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGAAGGGAAACGTGCTTGTTAACAGCAA  
 GTCCCAGACACCAGCCCCAGTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAG  
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGAGGAG  
 CCAGGCCGGGAGCAGGTGGTGGAAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA  
 TGGAGGGCCCTGAGCGAGACCAGTTGTCTATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
 GCCGGGGAAGGGAGAAAACAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG  
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
 AATCATACACTCTGAATTGAACTGGAATCACATATTTCAACAGGGCCGAAGAGATGACTA  
 TAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAATGTACATCTGA

**FIGURE 58**

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA  
VELKKNEFQGELEKQREQLDKIQSSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENNDQRQQQLQALSEPQPRLQAAGLPHTVEVPQGKGNVLGNSKSKTTPAPSSEVVLDSCR  
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPFVGGRGFGGAGELGQTPQVQAALSVSQ  
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND  
RNIDVFNVEDQKRDTINLLDQREKRNHTL

**Signal peptide:**

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**FIGURE 59**

GGATGCGAGAAAGCCTCAGTGTGCTCTTCTGCGCTGGGCTGCTTCTCTTCTACGCTGGCATTGCCCTCTTCA  
 CCAGTGGCTTCTGCTCACCCTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC  
 TGCCATGGGGAGCCAAAGGAAACCTGGGGCTTGTGGATGGCTTCCCGATTTTTCGCGGGTGTGTTGGTGCTGA  
 TAGATGCTCTCGGATTGACTTGCGCCAGCCCGCAGCATTACACGCTGCCTAGAGAGCCCTCTGTCTCCCTACCCT  
 TCCCTGGGCAAACTAAGCTCCTTGAGAGATCCTGGAGATTGAGCCCAACCTGCGCGCTCTACCCGATCTCAGG  
 TTGACCCTCTACCACCACATGACGCGCTCAAGGCCCTCACCACCTGGCTCAGTGCTACTCTTATTGATGCTG  
 GTAGTAATTCGCCAGCCAGCCATAGTGAAGACAATCTCATTAAAGCAGCTCACCAGTGCAGGAAGCGCTAG  
 TCTTATAGCCCCACAGCAGCTTCCCCAGCACCACCAGAGGAGCCAGAGTGATTCTCCTCAAGTTAGCCTTGTGC  
 CCACGCTGGCCCTGCTGCTGGGCTGCCATCCCATTTGGGAATATCGGGAGATGATGGCTGAGCTATTCTCAG  
 GGGGTGAGGACTCCCAGCCCCACTCCTCTGCTTAGCCCAAGCCTCAGCTCTCATCTCAGCTCAGCAGGTGT  
 CCCGATTCTTCTACTACTCAGCTGCTACTCAGGACCTTCAGCTAAGGAGCTCTATCAGCTCGCAACCTCT  
 TCTCCAAGCCCTCATCTACCTACTGCTGCTTCTCCAGAGCCCCAAGGGGCTGAGGCGCACTCCGACTGTGA  
 TTGCTGAGCTGCAGCAGTTCTGCGGGGAGCTCGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC  
 GCATGGCGGGGGTACTGCTCTTGGCTGCTTCCGTCTTATCTGCTCTGCTGGCATCTCAGTGGGCAATATCCC  
 CAGGCTTTCCATTCTGCCCTCTACTCTGACCTGTGGCTGCGGGCTGTTGGGCCATAGGCTATGCTGGAC  
 TCCTGGGAATATTGAGCTGAGCTAGATCTAGTGTCTTAGGGGCTGTGGCTCGAGTGAGCTCATTCTCCCTT  
 TTCTGTGGAAGCCTGGGCTGGCTGGGGTCCAGAGGCCCTGCGCAACCTGTTTCCCATCCCTGGGCGCGTCC  
 TGTACTCTGCTGTTTCTGCTTGGCTGTGTTCTTCTCTGATAGTTTGTGTAGCTGAGGCCAGGGCCACCCCT  
 TCCTTTTGGGCTCATTCATCCTGCTCCTGGTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC  
 TCACAATGCCCGCCTTGCGACTTCAGCCACAACAACCCCCACGGCACAATGGTGATATGCCCTGAGGCTTG  
 GAATGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTGGCCCTGAAGAGACACCTGTTTGGCACT  
 CCTCTCCCTGGCTGAGTCTCTGCGCATCCATGGTGGGTGGTGCAGGCCAAGAATTATGGTATGGAGCTTGTGTGG  
 CGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCGCTATGGTAATCTCAAGAGGCCCGAGGCC  
 CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATTGGGTACTGCTGCCACTTGGGCATTGGGCTCGGGG  
 CAGATGAGGCTCCCCCGCTCCCGGGTCTGGTCTCTGGGGCATCCATGGTGCTGCTCGGGCTGTAGCAGGG  
 TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTCTGGTGAAGGCTGGGGCAGGCGCTCAA  
 GGACCAGGACTGCTCCTACTCCCTTCTCAGGCCCCCCACTTCTCAAGCTGACTTGGATTATGTGCTCCCTCAA  
 TCTACCGACACATGCAGGAGGAGTTCGGGGCGCGGTAGAGAGGACAAATCTCAGGCTCCCTGACTGTGGCTG  
 CTTATCAGTTGGGAGTGCTACTGCTGCTATGGTACAGCCCTCACCTGTGGCCTTCCCCTTCCACTTCTGCTGT  
 TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTGCTTCTGTTTCTGCAAGAGCTTCTTCTCCTACATCTGCTTGTG  
 CTGGGATACCCGTCAACCCCCCTGGTCTTTTACTGTGCCATGGCAGGAGCTCTCGGCTTGGGCCCTCATGGCCA  
 CACAGACCTTCTACTCCAGAGCCACACGCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCTGTTGGGATTC  
 CAGAGGGTTCATGGCTCCTGACTTGGCTGCTGCTTGTGCTAGTGGGAGCCAAACCTTGGCTCCACCTCCTCT  
 TTGCAAGTGGTTGCCACTGCTGCTGCTGCGCTTCTGCTGTGAGAGTCAAGGGCTCGGGAAGAGACAGCAGC  
 CCCCAGGAATGAAGCTGATGCCAGAGTCAAGCCGAGGAGGAAGAGGACCTGATGAGAGATGCGGCTCCGGG  
 ATGCGCCTCAGCACTTCTATGACGACTGCTGAGCTGGGCTCAAGTACCTCTTATCTTGGTATTTCAGATT  
 TGGCCTGTGCTTGGCAGCCTCCATCCTTGCAGGCATCTCATGGCTCGGAAAGTGTGCCCCCTAAGTTTCATAT  
 TTGAGGCTGTGGGCTTCATTGTGAGCAGCTGGGACTTCTCCTGGGCATAGCTTGGTGATGAGAGTGGATGGT  
 CTGTGAGCTCCTGGTTCAAGCAGCTATTCTGCGCCAGCAGAGGTAGCCTGATCTGTGATTGGAATGGCCTGGCT  
 ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC  
 TCTTACTATCATGCAAGCCAGGGGCGCTGACATCTAGGACTCTATTATCTATAATTGAGGACCAAGTGGAGTA  
 TGATCCCTAAGCTCCTGATTGGATGATCTGAGGGAACAAGGGGGCGGCTCCGAAGTGGAAATAGGCCGG  
 GCGTGGTGACTTGCACCTATAATCCAGCACTTTGGGAGGCAGAGGTGGGAGGATGCTTGGTCCAGGAGATTCA  
 AGACAGCCTGTGGAACATAACAAGACCCGCTCTCTACTATTTAAAAAAGTGTAATAAATGATAATAT

**FIGURE 60**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW  
 MASRFSRVVLVLIDALRFDAQPPQHSHPVREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ  
 VDPPTTTMQRLKALTTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF  
 PGAFSKAFFFPFNFVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHPPEM  
 AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAALFLYSPTAVFPST  
 PPEEPEVIPQVSLVPTIALLLGLPIPFNGIGEVMALFSGGEDSQPHSSALAQASALHLNAQ  
 QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG  
 ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGFPPCPLLLTPVAWGLVGAIA  
 YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLA  
 VFFSDSFVVAEARATPFLGFSILLVVLHWEQQLLPKLLTMPRLGTSATNPPRHNGAY  
 ALRLGIGLLCTRLAGLFHRCPEETPVCHSSPWLSPASMVGGRAKNLWYGACVAALVALLA  
 AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP  
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE  
 EFRGRRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL  
 LLHLLAAGIPVTTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVPFAIHWHAFAVGFPEGHGS  
 CTWLPALLVGANTFASHLLFAVGCPLLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEEP  
 LMEMRLRDAPQHFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFI FEAVG  
 FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
 1016-1034, 1052-1070

**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT  
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**  
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT  
 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG  
 CCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTATGGAATGAATTTGACAAAA  
 GATTCTTTGTGCCTGCTGAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT  
 TCTAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAGCAGTGATGTATCCAGCCTTAA  
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
 GGTATGCTTCGCATTTGATGGAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCGGATAAAACAGTCATTGAATATGA  
 ATATGATGTGAGAACCCTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGAGG  
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCG  
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC  
 AAACCTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG  
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGT  
 TATATGTGCAGATGGAAAAC**TGA**TGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAC  
 AAGTGAGTCAACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT  
 TTGTCAAGTGTCTGTGAGAATTACTTATTTCTTTTCTATTCTCATAGCACGTGTGTGATTG  
 GTTCATGCATGTAGGTCTCTTAACATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT  
 GTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCGAATTTATTACAGG  
 TGGGTGT

**FIGURE 62**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNED  
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVRTTDICAGPEEQELSL  
QEEVSTQGTLLSQAAVLGPGTLOYSYTPQLQDLPLAQEHTDSEEGPEEPPSTTLVDWD  
PQTGRLCIPSLSSFQDSEGECEPSEGDLGEEGLLSRLYEAPDRPPGENETYLMQFMEEW  
GLYVQMEN

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCCCTCTGCTGACTGTGGCCACCGCCCT  
GATGCTGCCCCTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG  
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA  
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGGCCTGGTGGTGCTGGGCGCCACGTCCCTGAGTACTGCGGAGCCACCCAGCAGG  
TGTTTGGCATCGATGCTCTCACCACGCACCCGACTACCACCCCATGACCCACGCCAACGAC  
ATCTGCCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
TCGTGTCTGACTTTGAGGAGCTGCCGCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC  
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCCTCGTTTCTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCCGAC  
GTGTACACGCAGGTGTCCGCCCTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC  
CCAGCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT  
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
AAGCCTGATGTTTAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAAAAAAGAAA

**FIGURE 64**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF  
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC  
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD  
VCNSSWKGHLLTLMCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY  
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPFGAA

**Signal peptide:**

amino acids 1-30



**FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
 CGCCTGTCCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTGCGCGCTGGGCACGGTAG  
 CAGGCGCCGCGTGTGCTCAAGGACTATGTACCAGGTGGGGCTTGCCCCAGCAAGGCCACC  
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT  
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTTGGCGTTAAACCACCTGGGTCACTTTCTCTTGACAAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG  
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCTACT  
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCGCGGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
 GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT  
 TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGCCCCGAGGCTGAGGATGAGGA  
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
 GGGAGCAGCCCCTCCCCAGATAACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCACTACCTGAGCCGGGAGACCCAG  
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC  
 CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
 TGTGCACTTGACAGGCCACGTACAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC  
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
 TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTACAGCAGTGAGATGCTCAGAATAACTG  
 CTGTCTCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG  
 GGTGTTTGTCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC  
 GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA  
 TTGCTGGGACTCCACCTTCCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAAC  
 TTGCTCATTT

**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG  
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVVDILINN  
AGVMRCPHWTTEDGFEMQFGVNLGHFLLTNLLLDKLGASAPSRIINLSSLAHVAGHIDFDD  
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTNALHPGVARTELGRHTGIHGSTF  
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW  
AESARLVGLEAPSVREQFLPR

**Signal peptide:**

amino acids 1-17

**FIGURE 67**

GAAGTTCGCGAGCGCTGGCATGTGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC  
 CAGCGTGGCGCGCGCCCTGGCGCCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT  
 GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCAATTTACTCTCATCAAACGCCTGCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCAGGTTGTCTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACCGGCTCTTTTCTCTCA  
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATACCATGCC  
 ATTCCATGGCTGGAGGAGGCTGTCACTCTCTTCCGAGGATCTTACGGAGAGTGAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA  
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG  
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACCGTGGTAGC  
 TGAGGCTGTCTATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
 TATGTCAAGCCCTGGGTTCCAGCCCACTCTCTACCAAGATCCCTAGCCTCTACTGTTCCCTAT  
 GAGACCAATTCACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCACCTGGA  
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
 TTGCAGAACCATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAA  
 CCACCGCATTTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCAACAAGC  
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCCTGTGGTTAGGA  
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCTGTCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG  
 ACAGGAATTCGCGAGCCCTGCAGCTCCAGCCCTGAAGACTTGACTGTTGGCAGAGAGAAGC  
 TGGTGGAGTCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCACTTTGTCTGTGCCTCGCAAAATCAGAGGC  
 AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
 GTCAGAGTAGGATGCACAGTACAAGGAGGGGGGAGTGGAGGCTGAGAGGGAAGTTTCTGG  
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGGTC  
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
 GGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCACTGCCTTCTGCTGCAGCCCAAG  
 CAGGGAGTGTCCCCCTCCAGAAAGCATATCCAGATGAGTGGTACATATATAAGGATTTTT  
 TTTAAGTTGAAAACAACCTTTCTTTTCTTTTTGTATGATGGTTTTTAACACAGTCATTAATA  
 ATGTTTATAAATCAAAA

**FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS  
QPTLYQIIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLLSSVEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSSSPED

**Signal peptide:**

amino acids 1-19

**FIGURE 69**

GAGATAGGGAGTCTGGGTTTAAGTTCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG  
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG  
 CGCCAGGATGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCTACCTC  
 TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT  
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTGAAAGTGCCTTCC  
 TGGCTCCAGCCATCATCCTCATCTCCTGGGCGTCGTCATGTTTATGGTCTCCTTCATTGGT  
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTATGTACATCCTTGGGAT  
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACAGACCATTG  
 ACTTCTGAACGACAACATTGCAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
 AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCTTGACCCCTGGCCCTGTGGGGTGCCCTACA  
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACCTATCGAC  
 AAGGAGCGTTTCAGTGTGCAGGATGTCTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
 CTGGTTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
 TCTTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG  
 ATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCCACA  
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCTGTGTGTAGGTCCCACGGCCTCTGCCTC  
 CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT  
 GCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
 GAGCCTGAGGCTCTGCTCAGGGCCCATTTATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA  
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG  
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTTGGC  
 CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGGAGCCTA  
 GTTTTTTTTTTACGTGATTTTTGTAAACATTATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATCTTGCCCTTCCCCAACCAGTTTGTAA  
 TCAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAAAA

**FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863  
><subunit 1 of 1, 294 aa, 1 stop  
><MW: 33211, pI: 5.35, NX(S/T): 3  
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIIYAEVERQKYKTLES AFLAP  
AII LILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL  
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGV PYTCC  
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAV IIFWMDNYTIMACILLGILLPQFLG  
VLLTL LYTTRVEDIIMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGCTCTGGCATCCTGCACCTTGCTGCCCTCTGA  
 CACCTGGGAAG**ATG**GCCGGCCCGTGACCTTACCCTTCTCTGTGGTTTGCTGGCAGCCACC  
 TTGATCCAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
 GTCCTGAAGCACATCATCTGGCTGAAGGTATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCCTGGTCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC  
 AGGTTCATGAACCTCCTAGTGCCATCCCTGCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
 ATCGAGGCTTCCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTTC  
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTC  
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTAGCCTCATCGTGAGTCA  
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCTGTTGG  
 ACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA  
 GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC  
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
 ACTCCATCCTGTGCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG  
 AAGGCCTTGGGATTGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCC  
 AGCCTCCTTGTTGGAAACCCAGCTCTCCTGTCTCCAG**TGA**AGACTTGGATGGCAGCCATCAG  
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
 CAATAAACACTTGCCCTGTGAAAAA

**FIGURE 72**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881  
><subunit 1 of 1, 484 aa, 1 stop  
><MW: 52468, pI: 7.14, NX(S/T): 3  
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM  
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL  
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN  
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL  
GAKLLDSQGVKTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVL  
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPFEFFIDQGHAKVAQLIVLEVFPSSSEAL  
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL  
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLT PASLWKPSSPVSQ

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457



**FIGURE 73**

GAGCGAACATGGCAGCGGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTATCTGA  
 AAAGGTTAGTTCAGCTGATGGAATGGACTAAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCCGTCGCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT  
 CTCCAACATGCATAGACAGTGTGTGCTTTGCAAGCAAGCTGATGAAGAATCCAGATCCTGGC  
 AAACCTCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGGCATGGTGGATTGTTG  
 ATGAAGGCTCTGATGTATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT  
 CCTGCAAAAAGGGAACCCAAACGCGGTGATACATATGAGTTACAGGTGCGGGGTTTTTTCAGC  
 TGAGCAGATTGCCCCGTGGATCGCCGACAGAAGTGTGTCAATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCTTATGTGGGATTGCTTTTGGCTGTTATTTGGTGGACTGTGTAT  
 CTTGGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTTCAGCTTTTGTG  
 TTTTGTGCTTGTCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTGTA  
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTCTTTTATG  
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTGTATTATTTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTTCTGATGAGTTAAAAAAGGTCCTCAGAGATATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAAATCGTGTGTGTTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTAC  
 CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAGAAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT  
 CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAAATTGTAAAA  
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACACTACTTTAGTTAACTTGGTCATCTGAT  
 TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCTTGACCAGGTGTTCCACATATGCC  
 TGTTACAGATAAATACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTTCTTTTGTAGTAGAGAAATATGTGTGTGTCATGTGGTCTTCTGAAATG  
 GAACACCATTCTTCAGAGCACACGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCTT  
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTTAGAAA  
 GATTTTCAGATTCAATCCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAAATA  
 TAGCTTAGTGCTAAAATCAGTGTAACCTATACATGGCCTAAAATGTTTCTACAAATTAGAGT  
 TTGTCACTTATTCCATTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC  
 GAGGTGAGGAGTTTCAGAGCCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCACCTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

**FIGURE 74**

MAARWRFWCVSTMVVALIVCDVPSASAQRKKEMVLSEKVSQLEWNTNKRPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG  
SDVFQMLNMNSAPTFFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPYSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321



### FIGURE 75

[illegible]

**FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHPGSQVVKLPFINE  
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGVRTQ  
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW  
LRKEAINYTEPFVVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVS HDAIKIPKWSPLS  
EMHPVDYYSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY  
SSDHGELAMEHRQFYKMSMYEASAHVPLLMGPGIKAGLQVSNVVS LVDIYPTMLDIAGIPL  
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS  
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG  
QNYSNVIANLRWHQDWQKEPRKYENAIDQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG  
 GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
 GGTGGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG  
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
 TGTGACATCTATAGCACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
 ATCCTTGGAGGCCTCCTGGGATTCACTTCTGTTCCTGGAATCTTCATGGGATCCTACGGGA  
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTACTTGG  
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC  
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTCAATTCTACAGCCTGACAGGGT  
 ATGTGTTGAAAGAACAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG  
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
 CCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTG  
 ACTGACCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC  
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

**FIGURE 78**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886  
><subunit 1 of 1, 230 aa, 1 stop  
><MW: 24549, pI: 8.56, NX(S/T): 1  
MASLGLQLVGYYILGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT  
QCDIYSTLLGLPADIQAAQAMMVTSIAISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVF  
FILGGLLGFIPIVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLIAGIILCFSCS  
SQNRNSNYDAYQAQPLATRSSPRPGPPKVKSEFNSYSLTGYV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

[illegible]

**FIGURE 80**

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCPAPRCGDKIYNPLEQCCYNDAIVSLSE  
TRQCGPPCTFWPCFELCCLDSFGLTNDFFVKLVQGVNSQCHSSPISKCESRRRFP

Signal peptide:

amino acids 1-25

[illegible]



**FIGURE 81**

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGCCAGGACCCAGACGTGTGGAACACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA  
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTTAATGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCCTTCATT  
CTGTGACCTGTCTGAGGCCACCTGCGAGCTGCCCTGAGGAGGCCACAGGTCCCCCTTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCTTCACCTT  
TCTGTGAGATTTCCATCATCTCAAGTTCTCTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

**FIGURE 82**

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTFYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
 LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

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**FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCGCGCGCCGCTCCCGCCCGCTCCCGGCACCAGAAGTTCTCT  
 GCGCGTCCGACGGCGACATGGGCGTCCCGACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
 TCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC  
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTCACCCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GCGGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT  
 ACCCATCCTCCTCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCCAACCGCCGTGCCAGGAGCTGGTGC GGATGGACAGCAACATTCAAGGGATTGAAAACC  
 CCGGCTTTGAAGCCTCACCACTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG  
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCAGCAC  
 CCCCCGTCTCCTCCAGGCCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT  
 CTCCAACCTTTGAGGTATCTTAGCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTT  
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAACCCAGCCCTCAACCCCTC  
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAG  
 ATTCTCCCCTAGAGACCTGAAATTACACAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACACTGGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG  
 GAGAGACTTCTCCCCCGTGGCCGCCCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC  
 AGACTTCCTCTTTGTACCACAGTGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC  
 ACCTTCCCCAGCTGCCTCTACCAGAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
 ATATTGGGGCATGGTGGCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCCACCCACTGGAGATGGTGTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA  
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTA AAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

**FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFVATPYSLYVCPEGQNVTLTCRLLGPVDK  
GHDVTFYKWTYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD  
HHGNFSITMRNLTLDDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSSQ  
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRQELVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

**FIGURE 85**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
 TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTCGCCCTCC  
 TTTCTGCCCACCGTGCTTCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCCTCCGTGTCTTTTCGTCTCCCTTCTCCCGA  
 CTCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTC  
 TCCTCCTTGCTGGGACTCGCGTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC  
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT  
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACTGTCTCAGAGGGCGCCCATGTGAGT  
 TGTTACCGCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG  
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCC  
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC  
 CGCCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC  
 AACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT  
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTGCCTCCATGGGGTG  
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC  
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAAGGAGCAG  
 GCAGCACAACTGTCAAGATCGTCTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG  
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCCTG  
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCAGGT  
 ACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGGACAAA  
 GCAGACCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTCT  
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACTGCGTCGCTTTGCCCTGGAACACGAGG  
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG  
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC  
 GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGA  
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT  
 ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHP EKVAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRALEHEASDLVEIYLWKL  
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

**FIGURE 87**

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCC  
 GTGGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTCCCTTGCGGAAAATGCTGATCTCAGT  
 CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG  
 AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG  
 GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA  
 CGTGGCCTGGAGGAAGAACTGGATGGTTGGCGGCGAAGGCGGCCAGCGGGAGGTCACCGTT  
GAGACCGGACTTGCCCTCCGTGGGCGCCGGACCTTGGCCTGGGCGCAGGAATCCGAGGCAGCC  
 TTTCTCCTTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG  
 TCCTGTGAGCTGCCGTCCGGTGAGCACGTTTCCCCCAAACCTGGACTGACTGCTTTAAGGT  
 CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAC TGAAAGAACCAATAAAA  
 TCATGTTCTCCAA  
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**FIGURE 88**

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGEGGASGRSP

**Signal peptide:**

amino acids 1-18

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### FIGURE 89

[illegible]

**FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAAL EERLAQCQDQSSRHAAELRDFKNKM  
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETONPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDGTYISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVVPFPWVGTLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDTAQ  
QWDTPCPRENAEAAAFVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG  
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTTCTCCTTCTCTCTAATCCAT  
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGC GTTCTTCAGGGGCCAGTTCTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
 ACAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC  
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCACAGTCTTACTACCAGAAGGCCA  
 TCTGGGAGCTACAGGTGTGAGCACTGGGCTCAGTTCCTCTCATTTCATCACGGGATATGTT  
 GATAGAGACATCCAGCTACTCTGTGAGTCCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG  
 GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTGA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
 GCATTGTTGGACTGAAGATTTTCTCTCCAAATTCCAGTGGAAAATCCAGGCGGAACTGGAC  
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACAGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG  
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
 ATCATGGGTACTGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG  
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGT  
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAACCTCCC  
 ATAGTCATCTGCCAGTCAACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGCCTCTGC  
 AATCCCAGAGACAAGCAACAGTGAGTCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGG  
 GTGAAATG**TAG**GATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA  
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC  
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT  
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATAACACCTCTCAGGTGAAGAACCG  
 TCAGGAATTTCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTTCAGTA  
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**FIGURE 92**

MALMLSLVLSLLKLGSQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS  
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYQK  
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPQGDLSTDSRTNRDMH  
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
FGIVGLKIFFSKFQWKIQAELEDWRRKHGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKREFTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS  
PDHGYWVLRNLNGEHL YFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSQATT PFLP  
RGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

**FIGURE 93**

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCA  
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGGCGGAGCCGAGCGCGC  
**CATG**AGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCCGCCGCGCCGCCG  
 CCGTGCCTCAGCCGCCTCGGCGGGGAATGTACCGGTGGCGGCGGGGCCGCGGGGCAGGTG  
 GACGCGTCGCCGGGGCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTAGGGCGACGGC  
 TCCACGGCCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG  
 CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC  
 ACCACCTTTAGGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTC  
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTCGACGACCACTGGCCCCG  
 CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGACCCCGACCCCC  
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC  
 TTCGCCTCCTCCAGAGTATGTATGTAACCTGCTGTGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC  
 TGCAAGAGGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGAAGTGAAGTTTATT  
 TTATTTTAGCAAGGGAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
 GAGGATGAGGGTCATAGATTTACAAAATATTTATATACCTTTTATTCTCTTACTTTATATGT  
 TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAAGCACTAG  
 AGTCGCCAATTTTCTCTGGGATAATTTCTGTAATTTTCATGGGAAAAAATTATTGAAGAAT  
 AAATCTGCTTTCTGGAAGGGCTTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT  
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTGGTTTATTTTCTCTCTA  
 ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCATAATTTA  
 TTAACTAGTGGTAAGTAGACTGGTTTACTCTATTTACCAGTACATTTTGGAGACCAAAAG  
 TAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTGGAGGTAATTTAATCTAGTGGA  
 ATAATGTACTGTTATCTAAGCATTGCGCTTGTAAGTACTGCACTGAAAGTAATTTATCTTTGACCT  
 TATGTGAGGCACTTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT  
 AATGAAAAAATAATGACAGGTTTACTCAGTGAACCTGGGTATAACCCAAGATCTGCTGCG  
 CACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCTTTCACTGAGCTTGTTTCTCTCAAG  
 GTTGTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA  
 TTCTGGTTTGTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAATGTTTAAAG  
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTACTTTAGCACTAAATATTTTAAATGCTTTA  
 TAAATGATATTATACGTATTGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG  
 AGGCTGGGCGCGGTGGCTCACGCCTGAATCCTAGCACTTTGGGAGGCCAAGGCGGGTGGAT  
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCTCTACTAAA  
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACCTGTAGTCCAGCTACTCGGGAGGCT  
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGGCCACT  
 GCACTCCAGCCTGGTGAGAGAGGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 94**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

MRS LPS LGG LALLCCAAAAA VASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFP RATA  
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSPTTPPAAERTS  
TTSQAPTRPAPTTLSTTTGPAPTTPVATTVPAPTTPRTPTPDL PSSSNSSVLPTPPATEAPS  
SPPPEYVCNC SVVGS LNVNRCNQTTGQCECRPGYQGLHCETCKEGFY LNYTSGLCQPCDCSP  
HGALSIPCNR

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCCCTCACTCCAGAAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC  
CTGGGCTTCTGTGCAGTTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT  
CACAGCA

**FIGURE 96**

MGGLLLAAFLALVSVPRQAQAVWLGRDLDPQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRLTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

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**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
 GGCTGGATTTACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGAAGGGGCCAATACAGA  
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA  
 AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAG  
 GCACCCCTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG  
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC  
 CCGCTCCTCGGTGCTCACCCCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC  
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCCTGTGCCCC  
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
 ATTCACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAGCCACAGCCCTG  
 GTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTAGCCT  
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAGCT  
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
 ACAGATGAAGAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA  
 GAAGTCAGAGGCTGATTCTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
 CCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

**FIGURE 98**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF  
 REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
 SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS  
 PLDPSTTRSSVLTLIPQPDHGTSLTCQVTFPGASVTNKTVHLNVSYPPQNLMTVFQGDG  
 TVSTVLGNGSSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
 HLRDAAEFTCRAQNPLGSQQVYLNVSLSKATSGVTQGVVGAGATALVFLSFCVIFVVVRS  
 CRKKSARPAAGVGDTGIEDANAVRGSSASQGPLETPWAEDSPDPQPPASARSSVGEQELQYA  
 SLSFQMVKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATGA**AAGACCCTGTTCCCTG  
GGTGTACAGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCACGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC**TAGG**  
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCAAA

**FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

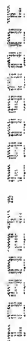
<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL  
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH  
MGKLVGRNSDTNREALLEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

**Important features:****Signal peptide:**

amino acids 1-17



**FIGURE 101**

GTTCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA  
TCCTGCTTGCTCTGGCAACAGGGCTTGAGGGGAGAGACCAGGATCATCAAGGGGTTGAG  
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG  
GGCGACGCTCATGCCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA  
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC  
AGCCCCCAGTTACGCCCTGCCTCACACCTTGCGATGCGCCAAACATCACCATCATTTAGACACCA  
GAAGTGTGAGAACGCCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGGCCCTCTGGTCTGTAACCACTCTCTT  
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC  
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA  
CCCACCACAGCCCATCACCTCCATTCCACTTGGTGTGGTTCCTGTTCACTCTGTTAAT  
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
CTGTCACTTAATAATCAACCTGGGGTTGAAATCAGTGAGACCTGGATTCAAATCTGCCTT  
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCAGCCCCA  
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 102**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH  
CLKPRYIVHLGQHNILQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTITW  
AVRPLTLSSRCVTAGTSCGISGWGSTSSPQLRLPHTLRCANITIIHQKCNAYPGNITDTM  
VCASVQEGGKDSCQGDGGPLVCNQLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

**Important features:****Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTTCGTGCGAGCCG**GATG**CCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA  
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGTTGTTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT  
TGCATACGGAAGGAAGGCTATGCAGAAGGCAAGATTCACCGGATGCTACATTGATTTTTG  
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAACTCATATCAGGATGCAGTTTTAGAAGATATTTTAAAGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT  
GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCCTATGAGAAGATATTTTGA  
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTGCAAACTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 104**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGVQVIKGLDIAMTDMCPGEEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDFKKNDHDGDFISPKEYNVYQHDEL

```

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214



[illegible]

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0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

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## **FIGURE 106**

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCNHGYTSGSGQKLFTFPL  
ETCNARHGG SRL

**Signal peptide:**

amino acids 1-18

106/249  
MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCNHGYTSGSGQKLFTFPL  
ETCNARHGG SRL

**FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC  
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**  
GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
TTCAATGGCACTGAGTGTGGGCGTAACCTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC  
CAGCCTGCGCTGCGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA  
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCCGTCCGCGTAACCAGCAGCGTTCAAC  
CCCTGCCCCTGCCCAATGACTGTGCAACCCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC  
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT  
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCA  
GCGGCGTCCCGGGGCAGGATGCCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA  
GTCCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**  
CTGTTTCCTCCACCTCCACCCCCACCCCTTAACTTGGGTACCCCTCTGGCCCTCAGAGACC  
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTGGCCTGGGAACCTTCTTGGAACCTT  
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

**FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPRNPPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17

108/249

**FIGURE 109**

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCGAGCTCAGCA  
 ACAGGTTCCAAGGAGGAAGGCGTTCTGGCTTGCTCAAAGCCCCGGCAGGAGAGGAGGCTGGCC  
 GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA  
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC  
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
 AAGATGATCTCAGAGGTGACAGGAGGGGTCACTGACACTATATCCTACCGAGACTTTGTGAA  
 CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**  
 GGACCCCGCCTGGACTCCCCAGCCTTCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
 CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTTGTTT  
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGCGGGGAATCC  
 TGAGCCTTGGGTCCCTCCCTCTCTTCTTCCCTCCTTCCCGCTCCCTGTGCAGAAGGGCTG  
 ATATCAAACCAAAAAGTCTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
 CTCACCTTGGAGGAACCAAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
 CTGCAGGGCCTCTTTCGGGTTTCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC  
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT  
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTTGGGAGCCCTTCAAGAAGG  
 TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG  
 GGGTTTGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
 CTGAGAAATACAAGGTTGCTTGCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFFEKEYMEFDLN  
NEGEIDLMSLKRMMKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV  
MFEGKANESSPKPVGPPPERDIASLP

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MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFFEKEYMEFDLN  
NEGEIDLMSLKRMMKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV  
MFEGKANESSPKPVGPPPERDIASLP

**FIGURE 111A**

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA  
GGAGCGGGGCGCTGCACACCATGGCCCCCGGGTGGGCGAGGGTTCGGCGCCGCGCTGCGCGCC  
CGCCTGGCGCTGGCCTTGCGCTGGCGAGCGTCTGAGTGGGCTCCAGCGCTGCCTGCC  
CACCAAGTGTAACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTC  
CTCGGGGATCCCCGCAACGCTGAGCGCTTGACCTGGACAGAAATAATATCACCAGGATC  
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGATCTGGAAGACAACAGGT  
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCTGAACA  
AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA  
GATTTGAGTGAAGAACAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCAGTGT  
GAAGAACCTGCAACTGGACAACAACACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC  
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG  
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT  
GCATGGCTCCTGTGCAATTTGAGGGGCTTCAACGTGGCGGATGTGCAAGAAGAAGGAGTACGTG  
TGCCCGAGCCCCCACTCGGAGCCCCATCCTGCAATGCCAATCCATCTCCTGCCCTTCGCC  
CTGCACGTGCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTTGCCA  
ACTTGCCGGAGGGCATCGTCGAATACGCCCTAGAACAAGAACTCCATCAAAGCCATCCCTGCA  
GGAGCCTTCAACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
TATTGCTCCAGATGCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA  
AGATCACCAGATTGCCAAGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
AATGCCAACAAGATCAACTGCCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT  
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCTCTGCAGT  
CCATCCAGACCTCACTTAGCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG  
CGCGACTACCTCGAGACAACCCCATCGAGACAAGCGGGGCGCTGCGAGCGCCGCGCGG  
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCGGCTGCTCAGGCTCCGAGG  
ATTACCGCAGCAGGTTGAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG  
TGTGAGGCGACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC  
TGAATATGTACCCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCGACTGGCA  
TCTTCAAGAAGTTGCCAACCTGCGGAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT  
GGAGACCGTGACCGGCGCGTGTTCGTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA  
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGTGAGACTGCTG  
TCCCTCTATGACAATCGGATCACCACCATCACCCTGGGGCCTTCAACACGCTTGTCTCCCT  
GTCCACCATAAACCTCTGTCCAACCCCTCAACTGCAACTGCCACTGGCTGGCTCGGCA  
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTCTC  
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCCGCGTGCCTGGAGCAGTGACCTGTATGGAGACAGTGGTGGAT  
GCAGCAACAAGGGGCTCCGCGCCTCCCGAGAGGATGCCAAGGATGTGACCGAGCTGTAC  
CTGGAAGGAAACCACTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGCTC  
ACCTCTCCACTGTATCCTGAGTACAACCGGCTGAGGTGCATCCCGCTCCACGCTTCAAC  
GGGCTGCGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCTGAAGG  
CTCCTTCACAGACCTCACATCTCTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG  
ACTGCACTCTTCGCTGGCTGTGCGAGTGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC  
CGCTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCGCTT  
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC  
CGTGCAAGAATAACGGGACATGACCCAGGACCTGTGGAGCTGTACCCTGTGCCTGCCCC

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCATCAACACCTGCATCCAGAACCCCTGTCA  
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTACAGTGCTCCTGCCCTC  
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
 AACAAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCCTAACTACAC  
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAGCATG  
 AGGCTCTGTGAGACAGACAATGATGACTGTGTGCCCCACAAGTGCCGCCACGGGGCCAGTG  
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTTCTGTG  
 AACACCCCCCACCATTGGTCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC  
 GGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG  
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACCTGG  
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAGGACAAC  
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT  
 GCGGTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGACAGTGTGGAGACAGTGA  
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCTGAACCTAGTAGTG  
 GACAAAGGAACTCCAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
 CCCCCCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCCTTGGCCAGGGCACGG  
 ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG  
 GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGCACCGT  
 GTGCAAGCAGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
 GCTGGACCGGCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC  
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG  
 GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG  
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC  
 GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAGGTGCCCATCATGGAATGTGCTGGGGGT  
 GTGGGCCCCAGTGCTGCCAGCCACCCGAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG  
 GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTT  
**CTAA**GGCCCTGCCGCTGCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
 ATGTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA  
 AGAGAATATTAAGTATATTGTAAAAATAAACAAAAATAGAACTTAAAAAAAAAAAAAAAAA  
 AAAAAA



**FIGURE 112**

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
 AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLKNLQVL  
 PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL  
 TLNNNNISRILVTSFNHMPKIRT LRLHSNHL YCDCHLAWLSDWLRQRRTVGQFTLCMAVHL  
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
 EIRLEQNSIKAIPAGAFQYKKLRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK  
 GLFDGLVSLQLLLLNNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL  
 AQNPFFVCDCHLKWLDYLDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS  
 SEC FMDLVCP EKKRCEGTIVDCSNQKLVRI PSHLPEYVTDLR LNDNEVSVLEATGIFKKLPN  
 LRKINLSNNKI KEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
 SNTDFAGLSSVRLLSLYDNRI TITPGAFTTLVSLSTINLLSNPFCNCHLAWLGKWLKRKR  
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRL  
 ALPRGMPKDVTELYEGNHLTAVPRELSALRHLLTIDLNNNSISMLTNYTFSNMSHLSTLIL  
 SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLAGTNPLHDCSLRWL  
 SEWVKAGYKEPGIARCSSPEPMADRLLLLTTPTHR FQCKGPVDINIVAKCNACLSSPCKNNGT  
 CTQDPVELYRCACPYSYKGKDC TVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR  
 CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVP ELNLCQHEAKCIPL  
 DKGFSCCEVPGYSGKLCETDNDDCAHAKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPPMV  
 LLQTSPCDQYECQNGAQCIVVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSPPTTVYSVETVNDGQFHS  
 VELVTNLNQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
 HGCIEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC  
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD  
 QGEFYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ  
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA  
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG  
GACAATTACTGGGGCTTCAGCCTTGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGTCTTGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAAACAACCACTGCCATGTCGCCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGA AAAAAGGCTGTGAGGTTTCC**TAA**ACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCTCATCTTGTCCCGTTTCCTCCCAATA  
TTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
TTAAATGTC

**FIGURE 114**

MKAAGILTTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
TVLDDGSIDYGIFQINSFAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMN  
YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

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**FIGURE 115**

CAGGCCATTTGCATCCCACTGTCTTGTGTTTCGGAGCCAGGCCACACCGTCTCAGCAGTGT  
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAACACTTGTACATGGCTCCC  
 CATTGGTTTTTTGGAGAAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC  
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCAGATCTGCTTCTCAC  
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA  
 ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAG  
 CTTTGACTCAGTTGTTCTGAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC  
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC  
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC  
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC  
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCCTGGAGT  
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCATTCTCAGAAGCA  
 ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAAATTTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC  
 TGCTGGTA**TAA**TCAGATTGTTTTTAAAGATCTCCATTAATGTCAATTTTTATGGATTGTAGACC  
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA  
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG  
 TCATTCCATGTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTCTGTCTA  
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA  
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT  
 CCACCGAAGTGTTCACTGTCATCTGTAGGGAATTTTGTGTTGTCTGTCTTGGCTGGATC  
 CATAGCGAGAGTGCTCTGTATTTTTTTTAAAGATAATTTGTATTTTGCACACTGAGATATAA  
 TAAAAGGTGTTTATCATAAAAAATAAAAAAAAAA

**FIGURE 116**

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFERLARRRKKILFYCHFDPDLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPKLD  
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRITSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV  
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF  
TEQLYRYVTKLLV

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**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTT  
 CGCCGTTACCTTCTTGTGTCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCAGAC  
 AAGCTGCAGGAATCCAGGGATTACTCCAACGAAGAAAAAGATGGTAATCTTCCAGATATT  
 GTGAATAGTGGAAGTTTGCATGAGTTCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT  
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT  
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT  
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTTCAGAAGAATTATTAGATA  
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT  
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG  
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGATGGGTCCAC  
 TTGATAAAAAACATGACTCGGAAAAAACAAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTTCAAGTCAACATATTTTTCATTGACTC  
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAAACCACCTCTGAA  
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTACTCC  
 AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAACTGTTGCAACTGCCA  
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATT  
 CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACTTTTTCCT  
 CACTTGGATTCTCAGGCACACAGGAGTGTCAGAGTTGAGGTTTGCATATATGGTGACCACA  
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
 AACAAAGTATGAAGTGGTAACATCATCAAGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
 ATTAAATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA  
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC  
 TTAA

**FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLDPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLVSVSLGTVDVLKQHINPNKTSDFETMLKSLRLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLLLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTWVSEIGKGFLDGS LDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQIILED SMIFSLASCIITAKLCTWAICFLTTS EEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRET LVLYALGVVL  
QDPNTWPSPHKFD PDRFDEL VMKTFSSLGFSGTQECPELRFAYMVT TVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCCGGACAGCAACAT  
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGG  
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGA  
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTGTCT  
TCTGCAGTGGCCCTTCAGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAA  
AAGAAACCCCTT**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
CCGCTTCGTATTCTTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA  
ATTAAAAAAAAAAAAA



**FIGURE 120**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPFTFTPEEYDKQDIQLVAALSVTLG  
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT  
EMALFVTVFGLKKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

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**FIGURE 121**

TCCCGGACCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
GTGCCCCGGAACGAGTGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC  
AGCAGGCCCCGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGACGTGGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC  
CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT  
CAGGGAGCCCTGAGGTCCAACCTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC  
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA  
ATAAAGATGTAGCTC

**FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

123/249

**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
 GACTCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCTCTCCCGGCTCAGAGGACCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCCCCCCATGGCCAATTCCACTCT  
 CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
 CGAACCCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCCGCGACCTC  
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACTACCATAGTGATACCCCTACTACCCATC  
 TGGG**TGA**CCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC  
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTCAGGCAGGGAGGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGAAGTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT  
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGTT  
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGTGGGGTGGGGC  
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC  
 ACAGCCCATCCGCGTGTGTGTGCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTACCTGTGACACCGGGTCTCTCC  
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGA  
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT  
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAGCTT  
 GCCCCGGGGCA

**FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521  
><subunit 1 of 1, 252 aa, 1 stop  
><MW: 28127, pI: 8.91, NX(S/T): 5  
MQLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR  
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPDYNHSDTPY  
YPSG

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 125**

GTGAATGTGAGGGTTTGTAGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA  
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG  
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
 TGGTGGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG  
 CATCTTCCCAGCACCAGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
 GGCTGCGGCTGCCCACACGGCTCACCATGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG  
 GCCGTGCTGCTGGTCTTACGCTGCCGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
 GCTCCTCTTCCCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCTTCTCG  
 GCGGTGCGGAGCACCAACCAGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
 CGATCAGATCCTGGTGAATGTGGGTAAATTTTTTACATTGGAGTCTGTCTTTGTAGCACCAA  
 GAAAAGGAATTTACAGTTTCAGTTTTTACGTGATTAAAGTCTACCAGAGCCAACTATCCAG  
 GTTAACTTGATGTTAAATGAAAAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC  
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
 AACTGGAGAAAGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTCTGGTG  
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG  
 AGTTATTGGAAGATCATTTTTTTCATATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG  
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCATTTCTGGGATTACTGAATTAGT  
 TACAGATGTGGAATTTTATTGTTTAGTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
 TGTTAATATATTGATTATATTTGTTTTATTCCCTTTGGAATTAGTTTGTTGGTTCTTGTA  
 AAAACTTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTAAAATAAGGTAATGAA  
 TGGCTTGCCCAAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTAAAAAAAAA  
 GAATGCTTCATAGTTGTATTTTAAATTGTATATGTGAAGAGTCATATTTTCCAAGTTATATT  
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG  
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACTTTATTGC  
 TCAACTTTAATTAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTT  
 TCCGTAGACATGACCACTTTATTAACGGTGGTGGGATGCTGTTGTTCTAATTATACCTAT  
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA  
 TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT  
 CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGATAAAGA  
 TTAATATATGTTAAAAAA

**FIGURE 126**

MSGRRALS AVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSSPLGI  
SVRAANSKVAFS AVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFVAPRKG IYSFSF  
HVIK VYQSQT IQVNLMLNGKPVISAFAGDKDVTREAA TNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

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**FIGURE 127**

CGGTGGCCATGACTGCGGCCGTGTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCTCATCGCCGGAGC  
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGCTCTGTCTC  
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG  
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTCCTTTATTCAGCTTTCATGAC  
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA  
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGCTCATGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
ACAAGAACTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA  
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG  
GTGGAATTGAGAAAGAAATAAACTATGCAGATA



**FIGURE 128**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

><subunit 1 of 1, 257 aa, 1 stop

><MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN  
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF  
GIMSGVFSFVNTLSDSLGPPTVGIHGDSPPQFFLYSAFMTLVIIILLHVFWGIVFFDGCCKKKW  
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCCLLCQDKN  
FLLYNQRRSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 129**

CGGCAACACGCGCGGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTTCGCTCTGGGCTTGCCCTTCT  
 TGGTGCTCTTGGTGGCCTCGGTGCAGAGCCATCTGGGGGTTCTGGGGCCCAAGAACGCTCTGCAGAAAGACGCCG  
 AGTTTGAAGCGACCTACGTGGACAGGTCACACAGCGAGCTGGTCAACATCTACACCTTCAACCATACGTGACCC  
 GCAACAGGACAGAGGGCGTGGCTGTGTCTGTGAACGCTCTGAACAGCAGAAGGGGGCGCGTGTGCTGTTTGGG  
 TCCGCCAGAAGCGAGCTGGGTGCTCTCCAGGTGCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT  
 ACCAAAAGTGAAGCAACCTGTGTGACGCCGCCACCAAGAATGAGTCGGAGATTCAGTTTCTCTACGTGGGATG  
 TGTCCACCTGTACCAGTCAACACACATACAGCTCCGGGTGAGCCGATGGACATTGTTGTCTCAGGACTG  
 GGGAGCAGTTGAGCTTCAATACCACAGCAGCACAGCCCGAGTACTTCAAGTATGAGTTCCCTGAAGGCGGTGGACT  
 CGGTAATTGTCAAGGTGACCTCCAACAGGCCTTCCCTGCTCAGTCATCTCCATTGAGGATGTGCTGTGCTGCTG  
 TCTATGACCTGGACAACACGTAGCCTTCATCGGCATGTACCAGACGATGACCAAGAAGGGGCCCATCACCGTAC  
 AGCGCAAGACATTTCCCAGCAACAGCTTTTATGTGGTGGTGGTGGTGAAGCCGAAGACCAAGCCTGCCGGGGCT  
 CCTGCTTTTCTACCCCTTCGCAGAAGATGAACCGGTGCATCAAGGGCACCGCAGAAAACCCCTGTGCTGCTGG  
 TGTCTCAAGCAGTCAGCTCTGAGGCATACGTGAGTGGGATGCTCTTTTGCTGGGTATATTTCTCTCCTTTTACC  
 TGCTGACCGTCTCTGGCCTGCTGGGAGAACGAGGGCAGAAGAAGACCTCTGGTGGCCATTGACCCGAG  
 CCTGCCAGAAAGCGGTCACTCGAGTCTCGCTGATTCTTTTCTGGGAGTTCCCTTATGAGGGTTACAACCT  
 ATGGCTCTCTTTGAGATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCATTGGGGACCTCTCTTACG  
 GTTACAGGGCGCGTCTTTTGAACCTGTAGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGAT  
 ACTACGACACATTGACCGACATCGATTCCGACAAGAAATGTCTTCGACCAAGCAATACCTCTATGTGGCTGACC  
 TGGCACGGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAGATCTACTCTGGAACATTGCCACCATGTGCTGTCT  
 TCTATGCCCTTCTGTGGTGCAGCTGGTGATCACCTACCAGACGGTGGTGAATGTACAGGGAACTCAGGACATCT  
 GCTACTACAACCTTCTCTGCGGCCACCCACTGGGCAATCTCAGCGCCTTCAACAACTCTCAGCAACCTGGGGT  
 ACATCTGTCTGGGCTGCTTTTCTGCTCATCTCCTGCAACGGGAGATCAACCAACCCGGCCCTGCTGGCGCA  
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTGGGCTTTTCTACGCCATTGGGCACAGCCCTGATGA  
 TGGAGGGGCTGCTCAGTGCTTGTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGACACATCTGTTACATGT  
 ACATGATCGCCGAGCTCGCATGCTGAAGCTCTACCAGAAGCGGCACCCGACATCAACGCGACGCGCTACAGTG  
 CCTACGCGCTGCTGGCCATTGTATCTCTCTCTGCTGGTGGGCGTGGTCTTTGGCAAGGGAACACGCGCTTCT  
 GGATGCTCTTCTCCATCATTCACATCATCGGCCACCCCTGCTCCTCAGCAGCAGCTCTATTACATGGGCGGTGGA  
 AACTGGACTCGGGGATCTTCCGCGCATCTCTCCAGTGCTCTACACAGACTGCATCCGGCAGTGACGCGGGCGCG  
 TCTACGTGACCGCATGGTGTCTGTCTGATGGCAACGTCTCACTGGTGGTGGCTGCTATGGGCTTATCA  
 TGCGCCCAATGATTTCGCTTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTTCGCTTCTACA  
 TCATCATGAAGCTCCGAGTGGGGAGAGGATCAAGCTCATCCCTGCTCTGCATCGTTTGACCTCCGTTGGTCT  
 GGGGCTTCGCGCTCTTCTTCTTCTTCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTCCAGGGAGCACA  
 ACCGGGACTGCATCTCTCGACTCTTCTGACGACCAGACATCTGGCACTTCTCTCTCCATGCCTATGCTTCG  
 TGTCTCTCTGGTGTGTTGCTGACTGGATGACGACCTGGATACGTGTGCAGCGGGACAGATCTATGCTCTTAGC  
 AGGAGCTGGGCCCTTCGCTTCACTCAAGGGGCCCTGAGCTCCTTTGTGTATAGACCGGTCACTCTGTCTGCT  
 GTGGGGATGAGTCCCAGCACCGCTGCCAGCATGGATGGCAGCAGGACGCCAGGTCTAGCTTAGGCTTGGCCT  
 GGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTTGCAGGAGCAGCCCTGCTCCCTTGAACCCCT  
 AGATGTTGGCCAAATGTGCTTCTTCTCAGTGTGGGCGCTTCCATGGGCGCTGTCTTGGCTCTCCATTT  
 GTCCCTTTCGAAGAGGAAGGATGGAAGGGACACCTCCCATTTTATGCTTGCATTTTGGCCGCTCTCTCC  
 ACAATGCCCGACCTGGGACCTAAGGCTCTTTTCTCCCATCTCCACTCCAGGGCCTAGTCTGGGGCTTGA  
 ATCTCTGTCTGTATCAGGGCCCGAGTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCCATTCAGTCAGCC  
 AGGATGGATGGGGGTATGAGATTTGGGGGTGGCCAGCTGGTGCAGAGTTTGGTGCTAAGGCCTGCAAGGGG  
 CCTGGGGCAGTGGCTATCTCTTCCCTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATT  
 TGAGAACCGCCTTCTGATTCAAGAGGCTGAATTCAGAGGTCACTCTTATCCCATCAGCTCCAGACTGATGACC  
 AGCACCAGGACTGGAGGGAGAAGCGCTCACCCCTTCCCTTCTTCTTCAGGCCCTTAGTCTTGCCAAACCC  
 AGCTGTTGGCTTCTCAGTGCCATTGACACTGCCAAGAATGTCCAGGGGCAAGGAGGATGATACAGATTGAC  
 CGCGTCTGCTCCACAGCTGTGGGCAACCCAGTGCTTACCTTAGAAGGGGCTCAGGAAGGATGTGCTGTTT  
 CCTCTACGTGGCCAGTCTTAGCTCTGCTCTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCAGTCTTCAGGCA  
 AGTTCTGTGTAGTCATGCACACATACCTATGAACCTTGAAGTTTACAAAGTCTGCCAGCTCTGGGCAC  
 CCTGGCCACCCTGGTCTTGGATCCCTCTGCTCCACCTGGTCCACCCAGATGCTGAGGATGGGGAGCTCAGG  
 CGGGGCTCTGCTTGGGGATGGAAATGTTTCTTCCCAAACCTGTTTATAGCTCTGCTTGAAGGGCTGGG  
 AGATGAGGTGGGTCTGATCTTTCTCAGAGCTCTCCATGCTATGTTGCATTTCGTTTCTATGAATGAATT  
 TGCATTCAATAAACACCCAGACTCAAAAAA

**FIGURE 130**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSDVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAFVIGMYQTMTKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFFYPFAEDEPVDQGHRQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLISYGYQGRSFEPVGT RPRVDSMSSVEEDDYDTLT DIDSDKNVIRTKQYLYVADL
ARKDKRVL RKKYQIYF WNIATIAVFYALPVVQLVITYQTVVNV TGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGFLFYAMGTALM
MEGLLSACYHVC PN YTNFQFDTSFMYMIAGLCMLKYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGN TAFWIVFSIIHIIATLL LSTQLY YMRWKLD SGIFERRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPND FASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWG FALFFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF

```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCAAGTGCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTG  
 ACC**ATGGT**CCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCAGAAAACTATGGTGGAAATTTCCCTTTATACC  
 TGACCAAGTTTGCCGCTGCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCA  
 GGCAAGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGACCAG  
 GGCCCTGGACCCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTCAACCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC  
 CTTCCTCTTCTTGAGGCTTCAGACCCGGGATGAGCCAGGCACAGCCAACCTCGGATCTTCGAT  
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGGAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCTTATACCCGCACCACATGGCCAGGTACACTGGAGTGGGGGTGATGT  
 GCACTATCACTGGAGAGCCATCCCCGGGACCCCTTTGAAGTGAATGCAGAGGGAAACCTCT  
 ACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCCATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA  
 TGACAACGTGCTATCTGCCCTCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGACTAGACTGTGACGAGAGGATGCAGATGCCCCGGCTCCCCAATTCC  
 CAGCTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
 GGTGGACCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA  
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCAGCTGT  
 GAAGTCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGTCTGCTCACTCCAGAT  
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCGCCTTCGCGCTCATGGATTTTGCCATTGAGAGGGGAGACACA  
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC  
 AGCGGGCTCTTCTGCTGACCATCCAGCCCTCCGACCCATCAGCCGAACCTCAGGTTCT  
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCCGGGGAGGTGCACACC  
 GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTGTGGAGGCCAGGA  
 TACAGCCCTGACTCTTGCCCTTGCCCTCCCAATACCTTGCACACCCCGCCAAGACCATG  
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGGCACGGTCCCTACAGC  
 TTCACCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCTCCAGACTCTCAATGGTTT  
 CCATGCCTACCTCACTTGGCCCTGCAATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG  
 TGGTCAGCCACAATCTGGCAGATGGCGAGCTCCTGGTTCCAGTGATGCTGTGCTCGCTGCAAC  
 GTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCACGAAGCTGTGCGC  
 AGTGGGCATCCTGTGAGGACCCCTGTGAGCAATAGGAATCTTCTCATCTCATTTTCAACC  
 ACTGGACCATGTCAAGGAAGAAGGACCCGATCAACCAGCAGACAGCGCTGCCCTGAAGGCG  
 ACTGTCTGA**AT**GGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTGAAGCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTCGAGAGCCTGGACACCAAC  
 TTTATGGACTGCCATGGGAGTGCTCCAAATGTCAAGGTGTTTGCCCAATAATAAAGCCCCA  
 GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

**FIGURE 132**

MVPAWLWLLCVSPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSDFQLEPRL  
GALALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSIESTWVSLEPIHLAE  
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN  
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSH  
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLP L RAGQNILLVLAMDLAGAEGGFSSTCE  
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE  
GTFGLDWEPPDSGHVRLRLCKNLSYEAAPSHV V V V V V QSVAKLVGPGPGPGATATVTVLVERV  
MPPPKLDQESYEASVPISAPAGSFLTTIQSPDPI SRTLRFSLVNDSEGWLCIEKFSGEVHTA  
QSLQGAQPGDITYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
TLGPNPTVQRDWRQLQTLNGSHAYLT L ALHWHVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV  
EGQCMRKVGGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTGAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACCTTGAAGCTCAATTTCTGAAATCTCCCTCCTCCT  
 TCAATCGGCCCTGTGGATGTCTGGTCCCATCTGTCAGTCTGCAGGCATTTAAATCCTTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA  
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATACTTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCCGAGACTTTCCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT  
 CAGCACTGGGAAAGGCGTGAGGCGGCCGGCCGTTTGGCTGAATGCAGGCATCCATTCCCGAG  
 AGTGGATCTCCCGAGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG  
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTGCTGTGGCCAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC  
 CTGGAAGCTCCTGCATTTGGTGTGACCCAAATAGAAACTGGAACGCTAGTTTTGCAGGAAAG  
 GGAGCCAGCGACAACCTTTGCTCCGAAGTGATACCATGGACCCACGCCAAATTCGGAAGTGA  
 GGTGAAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGCTTCATCGACCTGC  
 ACAGCTACTCCGAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC  
 GAGGAACCTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGGGCCACTGA  
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC  
 TTCTCTCTGCCAGCTAACCCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGGCGCATGGCTCTGCTCTGTCTACATTTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTTTGTGGAGACACAGGCCTGCCCTCTCTCAGCCAGTCTCCCTGGAGT  
 CGTGTGCTCTGGCGGTGCTCCCTGCAAGAACTGGTTCTGCCAGCTCTCAATTTTGGTCTCTG  
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCTGCTGGCTGGGCGGCTGCACTC  
 AGCATCACCCCTTCCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAACATC  
 TGAGATGATTCTTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTCTTAATTTT  
 TCGCAGTCTTCTTGAAAAATATTTTCTTTGAGCAGCAAATCTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTGTCTTGTGTGCC  
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTCACCACAACCTCTGCCCTCTGGGTTCAAGCA  
 ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA  
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCCA  
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
 TGCCGGGCCCTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCTCTTAC  
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTATTACAGTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTCAGGATGGTGAAATTATCCCATCTGTCTTAATGGGCTTACCTCCT  
 CTTTGGCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTTAAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCTGTGTT  
 TCCTTGTCTGGTTTG  
 TCTGTCTATTTTGTATCCTTGGACCAAGTTCTTAAGTAGAGCAAGAATTCATCAACCAGCT  
 GCCTCTGTTTTATTTACCTCAGCACGTACCATCTGTCTTTTGTGTGTGTGTGTGTGTGTGT  
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA  
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 134**

MRWILFIGALIGSSICQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR  
PVDVLVPSVSLQAFKSFRLRSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRPFAVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLPANQIIPTAEETWLGLKTIMEHVRDONLY

**Signal peptide:**

amino acids 1-16

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[illegible]



**FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAHLQGFQHLVHSLTVP  
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

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[illegible]

**FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVVISSGASTATNSGSSVTSSGVSTATI  
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE  
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT  
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS  
GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST  
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNHGAHRPRWSPNWFRRRPVSSIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
CCAGCAAT**ATGC**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
CTGTCTGGATGGGCGGCCAGCGATGACCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC  
ATGCCGGAAGGGAAGTGGAGAAGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
AAGGAGTTGGACAAAGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACTGGGGTCCAC  
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
GGCCTCAGTCAACACGCCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA  
TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTGCCGTTGTACATCAGCTGAC  
ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTG  
GGATTGTGAATAAACTTGATACACCA

**FIGURE 140**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG  
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG  
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN  
AHNGVNOASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

**FIGURE 141**

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCCGGCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGCC  
 CCGCGGGGGGCGGATGACCGTGGCTGACCTGACTCACTCCAGGTCGGGAGGCGGGGGCCCCGGGGCGACTCG  
 GGGGCGGACCGCGGGGCGGAGCTGCCGCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC  
 GCTCCTGCTCTCCGAATGCTGCGCACCCGCGATGGGCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCC  
 CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTCCTGCTGCGAGCCGCGCTCCGACTCGGGCGCTCAGC  
 CCCCCGATCAGCTGCTCTGGGCTCTGAAGAGCGGCCATTCCTCAGATTGGAAGCTGAACACACTCTCCAACTAC  
 ACAGCCCTTCTGCTGAGCAGGATGAGCAGCCCTGTACGTGGGTGCTCGAGAGGCCCTCTTTGACACTCAGTAGC  
 AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAACAGCAGTGC  
 AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACCTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC  
 CTGTTTCACTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAACTTCACCCCTGGCAAGG  
 GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGGCCGTGTCTCCTTCGACCCGAATTTCAAGTCCACTGCC  
 CTGGTGTTGATGGCGAGCTCTACACTGGAAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC  
 CAAAGCCTTCGCCCCACCAGACCGAGAGCTCCTCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCTCAGCCTAC  
 ATTCTTGAGAGCCTGGGCAGCTTGCAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA  
 TTTGAGTTCTTTGAGAACACCTTGTGTCCCGATTGCGCCGATTCGCAAGGGCGATGAGGGTGAGAGCGGGTG  
 CTACAGCAGCGCTGGACCTCCTTCTCCTCAAGGCCAGCTGCTGTGCTCAGCGCCCGACATGCTCTCTCCCTTCAAC  
 GTGCTGACAGGATGCTTTCAGCTGAGCGCCAGGCCCGGACTGGCGTGACACCTTTTCTATGGGGTCTTCACT  
 TCCAGTGGCACAGGGGAATACAGAAGGCTCTGCCGTCTGTGCTTCACAATGAAGGATGTGACAGAGTCTTC  
 AGCGGCGCTCTACAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG  
 CTTGGAGCGTGATCACCACAGTGGCCGGGAAAGGAAGATCAACTCATCCTGAGCTCCAGACCGCGTGCTG  
 AACTTCTCCTCAAGGACACTTCTGTATGAGCGGGGAGGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC  
 TACCAGCGGTGGCTGTACACCGCGCTCCTTGGCTGACACACACTACGATGTCCTCTTCTGGGCACTGGTGAC  
 GGCCGCGCTCCACAAGGCAGTGAGCGTGGGCCCCCGGTGCACATCATGAGGAGCTGCAGATCTTCTCATCGGGA  
 CAGCCCGTGCAGATCTGCTCCTGGACACCCAGGGGGCTGCTGTATCGGCCCTCACACTCGGCGGTAGTCCAG  
 GTGCCCTATGGCCAACTGCACACCTGTACCGGAGCTGTGGGGACTGCCTCCTCGCCGGGACCCCTACTGTGCTTGG  
 AGCGGCTCAGCTGCAAGCAGCTCAGCCTCTACAGCCTCAGCTGGCCACCAAGGCGGTGGATCCAGGACATCGAG  
 GGAGCCAGCGCCAAGGACCTTTGCAGCGCGTCTTTCGGTTGTGTCCCGCTCTTTTGTACCAACAGGGGAGAAGCCA  
 TGTGAGCAAGTCCAGTTTCAGCCCAACACAGTGAACACTTTGGCCTCGCCGCTCCTCTCCAACCTTGCCGACCCGA  
 CTCTGGCTACGCAACGGGGCCCCGTCAATGGCTCGGCCCTCCTGCCACGTCTACCCACTGGGGACTCTGCTGCTG  
 GTGGGCAACCAACAGCTGGGGGAGTTCAGTGTGCTGGTCACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC  
 TGCCCAAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCATTATCAGCACA  
 TCGCGTGTGAGTGCACAGCTGTGGCAAGGCCAGCTGGGGTGCAGACAGCTCTACTGGAAGGAGTCTCTGGTG  
 ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGCTTTTATTCTTGTCTTACCGGCACCGGAACAGCATGAAA  
 GTCTTCTTGAAGCAGGGGGAATGTGCCAGCGTGCAACCCAAAGACTGCCCTGTGGTGTGCTCCCTGAGACCCG  
 CCACTCAACGGCTTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGTTACAGTCCCTGTGACAGACCCCGG  
 GGGGCCCCGAGTCTTCTAGTGCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGAGGTTATCCCCAGTG  
 TGCCCCGGCCCCGGTCCGCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGACTGAGTCTTCCAGGAGACGC  
 TGCCCTTGGCTTCAAGGGGCTGTGAATGCTCGGAGAGGGTCACTGGACCTCCCTCCGCTCTGCTCTTCTGTTGAAC  
 ACGACCGTGTGGTCCCGGCCCTTGGAGCCTTGGAGCCAGCTGGCCTGTGCTCCTCAGTCAAGTAGCGAAGCTCC  
 TACCACCCAGACACCAACAGCCGTGGCCCCAGAGTCTTGGCCAAATATGGGGGCTCGCTAGGTTGGTGGAA  
 CAGTGTCTTATGTAACCTGAGCCCTTTGTTTAAAAAACAAATCCAATGTGAACATAGAATGAGAGGGAAGAG  
 ATAGCATGGCATGCAGCACACACGGCTGCTCCAGTTTATGCGCTCCAGGGGTGTGGGGATGCATCCAAGTGG  
 TTGCTGAGACAGAGTTGGAACCCCTACCAACTGGCCCTCTTCACTTCCACATTATCCCGCTGCCACCGGCTGC  
 CTTGCTCCTAGTGCAGGATCAGGACAGCTTGGGCTGCGTGCCTCTGCTGCTTGGCAGTCAAGCGAGGATGATGTTG  
 TTGCTGCGCTGCTCCACCACTTCAGGGACAGAGGGCTAGGTTGGGACTCGGGCCCTCACCAGGCTCTGGGCTC  
 GGACCCAACTCTGGACCTTTCAGCCTGTATCAGGCTGTGGCCACAGAGGAGCAGCGAGCTCAGGAGAGA  
 TTTCTGACAAATGTAGCCCTTTCCCTCAGAAATCAGGGAAGAGACTGTCCGCTGCTTCTCCGTTGTTGCTGTA  
 GAACCCGCTGTGCCCTTCCACCATATCCACCCCTCGCTCCATCTTTGAACCTCAAACAGGAGGAATTAACCTGACC  
 CTGGTCTCTCCCGAGTCCCGAGTTCACCTTCATCCCTCACCCTCCTCCACTTCAAGGATATCAACAGTGC  
 AGCACAGGGGCCCTGAAATTTATGTGGTTTTATACATTTTTTAATAAGATGCACTTTATGTATTTTTTAATAAA  
 GTCTGAAGAATTACTGTTAAAAA

**FIGURE 142**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF  
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP  
FDPNFKSTALVVDGELYTGTVSSFQGNPAISRSQSLRPPTKTESSLNLQDPAFVASAYIPE  
SLGSLQGDDDKIYFFFSETGQEFFEFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPFNVLQDVFTLSPPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG  
LYKEVNRETQQWYTVTHPVTPRPGACITNSARERKINSSQLPDRVLNFKDHFLLMDGQVR  
SRMLLLQPQARYQRVAVHRVPGHLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP  
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPNNTVNTLACPLLSNLATR  
LWLRNGAPVNASASCHVLPTGDLVLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ  
TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM  
KVFLKQGECAVHPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR  
PLSIQDSFVEVSPVCPRPVRRLGSEIRDSVV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

**FIGURE 143A**

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGGCCGGCTACGAAGAGGACGGGGACAGCGGCCGTGCGAACCGA  
GCCACGCCAGCCGGAGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCCCGCGTCTGCGCGCTCG  
TGCCGGCCCCCGGTCCCCGCGCGAGCGGGAGGAGCGCGCCGACCTCGCGCCGAGCGCCGCTAGCGCGCGC  
CGGGACATGGTCCCTCTTAAAGCGCGAGGCCGCGCGCGCGGGGGCGGGTGTGCGGAAACAAAGCGCCGCGCGGGG  
CCTCGCGGCGCGTTCGGGGCGCGCATGTGGCGCGGCGGGCCGCGCGCGCGCGCGCTCGCCGCGCGCGGCTCG  
CGGCGCTAGGGCGGGCTGCCCTCGTGGGCGGGGCGAGCGGGCTGAGGCGCGCGGAGCCTGCGCGCGCGCGGGC  
GGCGCGCGCGCGCGCGCGCGGGCAGCGCGCGGCG**ATG**CGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCAGCTGCT  
TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG  
GCCACGCCGCGCGCGCGAGCCCCGAGGGCTGCCGCTCGGGCAGGCGCGCGCTTCCAGGCGCGCGGGCGCGCG  
GCGATGCGCGCGGGGCGAGCTCTGCCGCGCGGCTCGGACCCAGATGGCGGCGCGCGCGCAGGAACTTTCTCT  
TCGTGGGAGTCATGACCGCCAGAAATACCTCGAGACTCGGGCCGTGGCGGCTTACAGAACTAGTCCAAGACAA  
TTCTCTGGGAAAGTTTCAGTTCTTCTCAAGTGAAGGTTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGG  
GTGTGGACGACTCCTACCGCCCCAGAAGAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA  
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAATCTTCTGAGGAGTT  
TGAACAGCAGCGAGGCCCTCTTTCTTGGGACAGACAGGCGTGGCGACCCAGCAAGAAATGGGAAATCTTCTGG  
ACGCTGGTGAGAGTTCTCTGATGGGGGCGCTGGCGTGATCATGAGCGGGAGGTGCTTCCGAGAAATGGTGGCGC  
ACATTTGGCAAGTGTCTCCGGAGATGATACACCACCATGAGGACGTGGAGTGGGAGGTTGTCTCGGAGTTTGG  
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTCAGAGCAGAAACAAAGGGGT  
ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATCACATTACCCCCAACAAAACCCACCTACCACT  
ACAGCTCCACAGGCTACATGCTGAGCGCGAAGATATCCGAGCTCGCCATCGCACAATACAGCTGCACCGCGAAA  
TTGTCTCTGATGAGCAAAATACAGCAACACAGAAATTCATAAAGAGGACCTCGAGCTGGGAATCCCTCCCTCTCTCA  
TGTAGGTTTCAGCGCCGCGAGCGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACATGTATTCGGCAG  
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCGCAGAGGGAAGCCTTGGACGACATTGTATGACAGTCA  
TGGAGATGATCAATGCCAACGCCAAGACAGAGGGCGCATCATGACTTCAAAGAGATCCAGTACGGCTACCGCC  
GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTCTGTGACAAAAGCACAAAGGGAAGAAAA  
TGACGTCCTCTGTGAGGAGGACGCGCTATTTCAGCAGACTTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC  
TGGATGCACAAAGATTGGCCAGAGAAATCAATCAGGAATCTGGATCTTGTCTTCTCTCAAACTCCCTGAAGA  
AGCTCGTCCCTTTTCAGCTCCCTGGGTCTGAAGAGTGAGCACAAGAACCCAAAGATAAAAGATAAACAATCTGA  
TCTCTTTGTCTGGCGTTTTCAGATGTTTGTGAGATTATGGGAAACCTTTGAGAGAGCTGCTTATCCCCATC  
AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCTTGACAGGCGCAACAAAGTTGAAGTATGA  
GAGATTACCGCATTAAGTACCTTAAAGCCGACATGCAGATTTTGCTGTGTCTGGAGAGTTTCAAGAGCCCTGG  
CCTCGGAAGTAGGATCCTCCCACTTTAACAAATGAATCTTGTCTCTCTCTGCGACGCTCGACCTCGTGTTTTCA  
CAGAATCTCTCAGCGATGTGAGCAAAATACAGTCTTGGGCAACAAATATATTTTCCAATCATCTCAGCCAGT  
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCAATTTTGCTTTACTCAGAAAACCTGGCTCT  
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCAGTGGTGGCTTTGATGTTTCCA  
TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC  
AGGAAGTAGGAGTAGTCACGCTCCACCATCTCTGCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT  
GCTTGGGGTCCAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCAA  
GTTACAGTAAAGCAGCAATAAATGGCTCAGTGAGGACAGCG**TAA**TGTCCAGCTTGTCTGGAAAAAGACGTTT  
TAATTATCTAATTTATTTTCAAAAATTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC  
AAGTGGTTTTCTACATAGGACTCCTTTAAGATTGAGCTTCTGAACAAGAGGTTGATCAGTGTTTGCCTTTGAA  
CACATCTTCTTGTGTAACATTATGTAGCAGACCTGCTTAACCTTGAATGAAATGACTCTGATGAACAAAACCTTT  
TTTAAAAAATGTTTCTTTTGAGACCTTTGTCCAGTCCATGAGCAGAAACGTTGAACATCTCTGCAAAAGTAT  
TATTGTAAACAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTGTTTAACTTCCACAGATTTCACTTTTGT  
GTTTGTGTTTTTTTTTTTACAATTTGTTTAAAGCCATTTTCATGTTCCAGTTGTGAAGATAAGGAAATGTGATAATA  
CCTGTTTTCATCATTTGCTTTCAGGAGAGCTTTCCAGAGTTGATCATTTCCTCTCATGTGTACTCTCAGCATGGC  
GAGTAGGTTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG  
CAGTGGCGCAATCTTGGCTCACTTTTAACTCCACTCCCTGGTTCAAGCAATTCCTCGCTTTGCTTCCCGAGT  
AGCTGGGATACAGGCACACACACAGCCAGCTAGTTTGTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG  
GCAAGCCAGCTGGCCAGTGTAGTTTAAAGCAAGGGCGGTGAAGAAGGCACATGAGGTATGTGGCTGTTCTCG  
TGGTAGTTCACTCGGCTAAATAGACTGGCATTAAATTCAGAAGAGTATTTGCAATTTCTCTTCTTGACCTT  
CTCTTTAAGGGTAAAATATTAATGTTTGAAGTACAAAAGATGAATATTATCAATAAATCTGATGTACACAGACT  
GAAACATACACACATACACCTTAATCAAAACGTTGGGGAAAAATGTATTTGTTTTGTTTTGTTTTGTTTTGTTTTG  
TGTTATGTGGGTGGAGATGGTTTTTCACTCTGTTTCACTACTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG  
TTTATTTAATATCTGTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTTATTTATGTGTATCGG  
GAGTGTGTTTAGTCTGTTTTATTGTCAGTAAACCGATCTCCAAGATTTCCTTTTGGAAACGCTTTTTCCCTCC



**FIGURE 143B**

TTAATTTTATATTCTTACTGTTTTACTAAATATTAAGTGTTCCTTGACAATTTGGTGCTCATGTGTTTTGGG  
GACAAAAGTGAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT  
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG  
CCTGATGCTCATTTGGAAAAATAAACCAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCCTCATT  
ATTCCGTGTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAATTAACACGAAAAAA

145/249

**FIGURE 144**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEG  
SDTSVPPIPVVPLRGVDDSYPPQKKSFMMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLLENFLR  
SLNSSEPLFLGQTGLGTTEEMGKLALFGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT  
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLEHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE  
ILEWEFLTGKYLYSAVDGQPFRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNPMYGAEYILDLLLLYKHKHGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKPKDKKINILIPLSGRFDMFVRFMGNFEKTC  
LIPNQNVKLVLFFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ  
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH  
VHHPVFCDPNLDPKQYKMCGLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
 TTTGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
 ACGGACGACGCCT**ATGA**AGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG  
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAAACTTGAATCATTATATA  
 CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC  
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA  
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA  
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC  
 ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC  
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
 CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGGAAGCACCCAGAGAGTTGGAATAAT  
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA  
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC  
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTA AAAACAATGTATAAGTCCCAGTTATTGCCA  
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC  
 TAGATCTAAACTCTATGAATATTTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG  
 CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
 AAAGTTTAT**TAA**ACAATAATATAAAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA  
 TTTAAGCAAACCTGCATTTTTCACAGGAGAAATAATCATATTGTAATTTCAAAGTTGTAT  
 AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA  
 ATTTTCATATGCACTAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAAA

**FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK  
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTTFPTGGFTPEIGKKKHTESTPFWSI  
KPNNVSIVLHAEOPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK  
STGIEISTESEDVPLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNP  
AYREDIEASKDHLKRLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL  
YEYLDIKCVPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19

**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCCAAATCATCCATCCACCCCTGCTGTCTATCTGTTTTCATAGTGTGAGATCAACCCACA  
 GGAATATCC**ATGGC**TTTTTGTGCTCATTTTTGGTTCTCAGTTTTCTACGAGCTGGTGTGAGGACA  
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCCTGTTCTTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
 GTATCGAGGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC  
 TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCACTTCCCAGATTTTAC  
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC  
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCTATGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTGTCATGGGATGATAATTGTTTTCTCAAATCCAAGGGGAAAATCCA  
 GGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGGAAACACG  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA  
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTAAGGGAGGTGGACGTGGGAC  
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG  
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAAACAGAACATTTGTATTTTAC  
 ATTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCTACACGAGTAGGGGTCTTCC  
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTATACC  
 CTGCTGACATGTCAGTTTTGAAGGCTTGTGAGACCCTATATCCAGCATGCGATGTATGACGA  
 GGAAAAGGGGACTCCCATATTCATATGTCCAGTGTCTGCGGAT**TGA**GACAGAGAAGACCCTG  
 CTTAAAGGGCCCAACACCAGACCCAGACACAGCCAAGGGAGAGTGTCCCGACAGGTGGC  
 CCCAGCTTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC  
 TGAGGTTCTTCTGCCCCGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT  
 TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
 CATTAGGTTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTGCTCACAGGTGAAGATTAAGAGA  
 CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCACAGTGTGTTGCTAATGATGTGTTTTTA  
 TATTATACATTTTCCCACCATAAACTCTGTTTGCTTATTCCACATTAATTTACTTTTCTCTA  
 TACCAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAGAG  
 GAGGTAGGATTTTCACTGATTCTATAAGCCCAGCATTACCTGATACAAAACAGGCCAAAG  
 AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAACACAGACACAAAAA  
 TTCTAAATAAAATTTTAACAAATTAACATAAACAATATATTTAAAGATGATATATAACTACT  
 CAGTGTGGTTTTGCCACAAATGCAGAGTTGGTTTAATATTTAAATCAACAGTGTAATT  
 CAGCACATTAATAAAGTAAAAAGAAAACCATAAAAA

**FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC  
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYEVDVGQNVGWYVGVCRDDVDRGKNNVTLS  
PNNGYWVLRLLTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT  
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

**FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTTGTGTGGGAACCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAGAAGACCTACAA  
 TTAATAAGCATTGTTCATTACAACTGACAACTATATGCTGAGTTTGGCAGAGAGGGCTT  
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
 TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAACTGTAG  
 ATAAAATTGTTCAACTTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA  
 GATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAG  
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA  
 GAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG  
 GTCTCCGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT  
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA  
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG  
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA  
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT  
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
 TGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
 CCAGATCAACTCTGTCTCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTCAGAATTTTGAC  
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC  
 AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAAAGGAGTGAAGAAAATA  
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC  
 ACTTCATCATTTAGGAAGTATGGGAAGTAAAGTAAAGTCCAGAAAGAAGCCAAGATATA  
 TCCTTATTTTCAATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
 ACCATAATAAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

**FIGURE 150**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD  
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR  
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL  
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG  
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDV  
MFVTGFGALKNDGYSQNHRLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD  
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)



**FIGURE 151**

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
CGTGACCTTCTTGGTCCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG  
CAGATGAGACTGAGACGGCGTGGCCGCCCTTTGCCGGCTGTCCCTGCGACTACGACCCTGCG  
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGCCTGCCCTGTGCCC  
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCCTCCACTACTGG  
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGGCCCCCGCTGAACGCTACGGTCCG  
CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGGCATTATGTCTGTTGCGTAGTGGCCGCTA  
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
CCTGCCTTCGGGCCTTGCAAGCCGCTTGCGGTGCCGCCCAACCCCCGCACTCTGTGCCACGC  
GGCCGTGCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
GCCTGCGGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTC**TGA**  
AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
GGCGCTTTGTTTCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTTTA  
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 152**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL
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**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

**FIGURE 153**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCCGATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGG  
 CCCAGCGCCGACGATCCGTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC  
 TTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT  
 CTACGCCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTTCTGCTTGGGA  
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC  
 ATTTTGACTTACTTTCCGTGTGGTTCATCCGGTCATGATTGCTGTTTGTCTGTTTCTTATCAT  
 TGTGGGGATGTTAGGATATTGTGAACGGTAAAAGAAATCTGTTGCTTCTTGATGGTACT  
 TTGGAAGTTTGTCTGTCATTTTCTGTGTAGAAGTGGCTTGTGGCGTTTGGACATATGAACAG  
 GAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAGT  
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCCAGAT  
 TCCTGCTGTGTTAGAGAATCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGA  
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTGAGAGGAACCAAACTGC  
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAATCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC  
 CTTGAAGAATGACAACTCTCAGCACCTGTCTGTCATGTCCCTCAGTAGAACTGTTGAACCAAGCC  
 TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG  
 GAGTTATAAAGAAATGTACAGAAGAAAACCAAACTTGTTTATTGGACTTGTGAATT  
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAATAAAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTTAAAAATGAGGATGGAAAAGTTTCATGTCATAAGTCCAC  
 CACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT  
 CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT  
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTTC  
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAAATATTCTTACCACTTAAAA  
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA  
 TCTGTATAATTCACTGATTTTCACTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
 ATTTGTCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTTACTATTCTGT  
 CCTGGGCTTATATTACACATATACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA  
 CCAGTGTGATACATAGGAATCATTATTGAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAA  
 GAAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTTGTATGCTGTTTTTCTCCCAATG  
 AAGACTCTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA  
 GCAATAGTCTCCAAGTCAATATAAAATCTACAGAAAATAGTGTTCTTTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATTAACATGTGACAATTTAGAGATCTTTTGTGTTTATTTCACTGATTA  
 ATATACTGTGGCAAATTACACAGATATTAAATTTTTTACAAGAGTATAGTATATTTATTT  
 GAAATGGGAAAAGTGCAATTTTACTGATTTTGTGATTTTGTGTTTATTTCTCAGAATATGGAA  
 AGAAAATTAATGTGTCAATAAAATTTTTCTAGAGAGTAA

**FIGURE 154**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV  
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTYEQELMVPVQ  
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF  
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL  
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

**FIGURE 155**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC  
 TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGAATTCTGACCTGCTGGCCAGCCAGGA  
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
 ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG  
 TGATTCTGGATAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG  
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
 CCCCAGGGGCTGCACTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
 ACTCGGCCACAGGGAACGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG  
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA  
 TGTGTGTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTC  
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCCGT  
 GTGGTGGGTGGGGAGGAGGCCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGA  
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACT  
 GCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC  
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAA  
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGC  
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA  
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
 GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA  
 TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC  
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG  
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCCTTTCAGAGTCTGGGAGCCGCTTCCTTCCTG  
 CCCTGCCCACTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC  
 CTCTGCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCC  
 TCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC  
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA  
 GGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGCCAGATCACTGTGGG  
 CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA  
 CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
 ACCTACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT  
 CTGGCAAAAAAAAAA

**FIGURE 156**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPITIIALLSLASIIIVVVLIKVILDKYYF  
 LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF  
 SACFDNFTEALAETACRQMGSRAVEIGPDQDLVDVEITENSQELMRNNSGPGCLSGSLVSL  
 HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDV  
 FNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNNDIALMKLQFPLTFSGTVRPICLPFFD  
 EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE  
 GGVDTCQGDSSGGLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

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**FIGURE 157**

GGGCTGAGGCACTGAGAGACCGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCAGGCTCCAG  
 AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCC  
 TTTTCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGGCGGGCAGGGGCCCATGCCCA  
 GGGTCAGATACTATGTCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCTCCAGGATTTTGACA  
 CTCTGCTCCTGAGTGGTGATGGAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGG  
 ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA  
 AGAAGAAGAGCAATGAGACACAGTGTTTTCAACTTCATCCGTGTCTGGTTTTCTTACAATGTACCCATCTCTACA  
 CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCTACCTGTTGCCATCTCGG  
 AGGACAAGGTCTATGGAGGAAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG  
 GGATGCTCTATTCTGGTACTATGAACAACCTTCTGGGCAGTGAGCCATCCTGATGCGCACACTGGGATCCAGC  
 CTGTCTCAAGACCGACAACCTTCTCCGTGGCTGCATCATGACGCCCTCTTTGTGGCAGCCATCCCTTCGACCC  
 AGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  
 CTAGAGTCTGCAAGAATGACGTGGCGCGGAAAAGCTGTGTCAGAAGAAGTGAGACCACCTTCTGAAGGCCAGC  
 TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCTGCTCCCCGCGATTCTCCCA  
 CAGCTCCCCACATCTACGCAGTCTTCACTCCAGTGGCAGGTTGGCGGGACCGAGAGCTCTGCGGTTTGCGCT  
 TCTCTCTCTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTACGCTGGACTA  
 CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGATAAGGCCCTGACCT  
 TCATGAAGGACCATTCTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTGAATCTGGCGTGGAGTATA  
 CACGGCTTGCACTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCTGATGTAAGTGGGAACACACAG  
 GGTCCCTCCACAGGCTGTGGTAAGTGGGACAGCAGTGTCTATCTGGTGGGAAGAGATTGAGCTGTTCCCTGACC  
 CTGAACCTGTTGCAACCTGCAGCTGGCCCCACCCAGGGTGCACTGTTTGAGGCTTCTCAGGAGGTGTCTGGA  
 GGGTGCCCCGAGCCAACCTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGCCCGGGACCCCACTGTGCCT  
 GGGACCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG  
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTTGGCCCTCAGAGCCGCCCAACATCATT  
 AAGAAGTCTGGCTGTCCCCAACCCTCATCTGGAGCTCCCTGCCCCACCTGTGAGCCTTGGCCTCTTATTATT  
 GGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGTCTGATAGTGCAGG  
 ATGGAGTTGGGGTCTCTACAGTGTGGCAACTGAGAATGGCTTTTCATACCTGTGATCTCCTACTGGGTGG  
 ACAGCCAGGACAGACCTGGCCCTGGATCTGAACCTGGCAGGCATCCCCGGGAGCATGTGAAGTCCCCTTGA  
 CCAGGGTCAGTGGTGGGGCGCCCTGGCTGCCAGCAGTCTACTGGCCCCACTTTGTCACTGTCACTGTCTCT  
 TTGCCTTAGTGCTTTCAGGAGCCCTCATCATCTCTGTCGCCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG  
 TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGCTTAAGCAGAGAGCAACACCTCCAGTCTCCAAGG  
 AATGCAGGACCTCTGCCAGTGTGTGGACGCTGACAACAACCTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  
 CAGGCCGGGGCTGCGGTGCAGGCACTGGCCATGCTGGCTGGGGCGGCCAAGCAGACGCCCTGACTAGGATGACAG  
 CAGCACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG  
 ATGCACAGCAGTCTGCCTCCCCATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCTAC  
 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGACCCCTC  
 CAGAAACACAGTGTTCAGAGACCCCTAAAAACCTGCCTGTCCCAGGACCTATGGTAATGAACACCAACATC  
 TAAACAATCATATGCTAACATGCCACTCTTGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT  
 TCTCCAGGGTCATGCAGGATCTGCTCCCTCTGCTTCCCTTACCACTGCTGCACCGCTGACTCCCAGGAAGTC  
 TTTCTGAAGTCTGACCACCTTTCTTCTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCCTGGCAGAATGG  
 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTCTTCTTGT  
 TTTGGGATTCAAAAACCTGCTTGTGAGAGACTGTTATTTTTATTAAAAATATAAGGCTTAAAAAA

**FIGURE 158**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSFHKGGLQ  
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVRLKNMIPWPASDRKKSECAFKKKSNETQC  
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHHTA  
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE  
ETASEFDDFERLHTRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL  
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET  
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM  
YLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFGSGGVWRVPRAN  
CSVYESCVDCLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP  
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGG  
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP  
HFVTVTVL FALVLSGALIIIVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT  
SASDVDADNNCLGTEVA

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704



**FIGURE 159**

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
 TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCTGCTC  
 TCAGAGGCTGCCAAAATCCTGACAAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG  
 GTCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGAATTCTTCTGGAAGAACTTTAGG  
 TGGCAGAGGAAAATTTGAAAACCTTATAAATGTTCTAGAATACTGGCGTTGCAGTGCAGTC  
 ATTTTTTAAATAGAAAGGATATCATGGATTCCCTAAAGAATGAGAACTTCGACATGGTGATA  
 GTTGAAACTTTTGACTACTGTCTTCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC  
 CATTCCTTCCACTTCATTCCGCTCTTGGAAATTGGGCTACCAATCCCCTGTCTTATGTTT  
 CAGTATTCCTTCTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTG  
 ATGTTCTTTAGTTTCTGCAGGAGCAACAGCATGCAGTCTACATTTGACAACACCATCAA  
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTTCAATTAACCTGACTTTGCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT  
 GTTGGAGGCTTGATGGA AAAACCTATTAAACCAGTACCACAAGACTTGGAGAATTCATTGC  
 CAAGTTTGGGGACTCTGTTTTGCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA  
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCACCCCAAGGGGTGATATGG  
 AAGTGTCAAGTGTTCATTGGCCAAAAGATGTCCACCTGGCTGCAAATGTGAAAATTTGGA  
 CTGGCTTCTCAGAGTGACCTCCTGGCTCACCAAGCATCCGTCTGTTGTGACCCACGGCG  
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT  
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTTTTCTATTCAAGTT  
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTCTATCTGCGCTCCCACCCGCTCAGCCCCACACAG  
 CGGCTGTGGGTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA  
 TGTCTTTAGCAGCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTCTGCTGGGGC  
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACA**TAA**GGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG  
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCTCTT  
 TAGTTATCTCTCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAATCATCTTTCCACTTGC  
 TAATTTTGTCTACAAATTCATCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCTT  
 CTTGTCTCTCTTGTTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
 GACCACTGACCCTCAGATTTCCAGCCTTAAATCCACCTTCTCTCATGCGCCTCTCCGAA  
 TCACACCCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTTCTTTCAGTTTCTGTTT  
 TGTTCTCCCATATTTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAAGGC  
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGGCCACAGTGAGTCTCT  
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACA  
 CGTTATCTCTCCCCAACCTCACTAA

**FIGURE 160**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSHLLLKAELWFINSDFAFDFARPLLPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP EIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPVMGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVFLGLTLGTLWLICGKLLGMAVWVWLRGARKVKET

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

**FIGURE 161**

GGGCTGTTGATTTGTGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACATACCATGTT  
 CTCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGGTACCCCTGAAGCTCT  
 GGTGTCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCAAAGCCCA  
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAACCTGCAGTGACAGCAGGAGTAAGAGT  
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGTTTCAGCGAGCCTAGAGAGGGC  
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA  
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC  
 TACCAGGTCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC  
 GGGTGGGCCCAGGAGGGGTGAGAGCCGTCCTGCTGGAGGGGAGTGCCTGGTGGTCTGTGA  
 GCCTGGCCGAGCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC  
 GAGTGGCATTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
 ACCAGTGGGGCCATCTACTTCGACCAGGTCCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC  
 CTCTGGCTCCTTCGTAGCCCCGTGTCGGGGGTGTCTACAGTTCCGGTTCCATGTGGTGAAGG  
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACAGTGGCCTGTCTATCTCAGCC  
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTCTACTGCCCTTGA  
 CCGTGGGACCGAGTGTCTCTGCGCTGCGTGGGGGAATCTACTGGGTGGTTGGAATACT  
 CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTTGAGGACCCAAAGTCTTTCAAGCACAAGAAT  
 CCAGCCCTGACAACTTTCTCTGCCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG  
 ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCCTGTGCCAAACACCCAGTTTAA  
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCACTTACC  
 CTCCCAGCCACCTGCTGCATCTGTTCCCTGCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA  
 AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCACCCAGCTTCCT  
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAG  
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC  
 TCAGCCAGCACCGTCTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC  
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAAGGAAGGAGGGTGTATTG  
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
 GGCTGTCTTCTATGCTGGATCCCAGATGGAATCTGGCCCTTACCTCCCCACCTGAGATTAG  
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGCCACCTCTGAAACTGCTCCAC  
 CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCTCTCCAGCTCTC  
 TCACTGAGTTATCTTCACTGTACCTGTCCAGCATATCCCCACTATCTCTCTTTCTCTGAT  
 CTGTGCTGTCTTATTCTCTCCTTAGGCTTCCTATTACCTGGGATTCATGATTCACTTCCTT  
 CAGACCCCTCTCCTGCCAGTATGCTAAACCCCTCCCTCTCTCTTTCTTATCCCGCTGTCCCAT  
 GGCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCACTGAGACACTAT  
 AGAATTACTAAGGAGAAGATGCCCTCTGGAGTTGGATCGGGTGTTACAGGTACAAGTAGGTA  
 TGTTCAGAGGAAAATAAATATCAAAGTGTATACTAAATTAATAA

**FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLERGECLVVCEPGRAAAGGPGGA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG  
NLLGGWKYSSFSGFLIFPL

**Signal peptide:**

amino acids 1-32

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[illegible]

**FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS  
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVDWNTPKKGRRS  
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHHPHGIMGLGAFCNFSTEATEVSKKFP  
GIRPYLATLAGNFRMPVLRREYLMMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGGAESLSSM  
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA  
PCIFHGRGLFSSDTWGLVPYSPITTVVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK  
HKTKFGLPETEVLEVN

**Important features of the protein:****Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

**FIGURE 165**

GGGCGGCGGGATGGGGGCGGGGGCGGGGCGCCGACTCGCTGAGGCCCCGACGCAGGGCCGGGGCCGGGCCA  
 GGGCCGAGGAGCGCGCGGCCAGAGCGGGGCGCGGAGGGCGACGCCGGGGACGCCCGCGACGAGCAGGTGGCG  
 GCGGCTGCAAGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCTTGGGA  
 CGGCTGTCTCAGCAGGGGGCCGTGCACCCGCTCCTGAGCAGCGCCATGGGCCCTGCTGGCCCTTCTGAAGACCCA  
 GTTCGTGCTGCACCTGCTGGTGGCTTTGTCTTCTGCTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC  
 GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA  
 ACTGGTCATGCTGCTGGAGTGGTGGTCTGCACGGAGGTACACTGTTACGGACCAGGCCACGGTAGAGCGCTT  
 TGGGAAGGAGCAGCAGTCATCATCTCAACCACAACCTCGAGATCGACTTCCTCTGTGGGTGGACCATTGTGTGA  
 GCGCTTCGGAGTGTGGGAGCTCCAAGGTCTCGCTAAGAAGGAGTGTCTACGTGCCCTCATCGGCTGGAC  
 GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTCGAAGGGCTGAG  
 GCGCTGTGGACTACCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACCGGCTTCACGGAGACCAAGCA  
 CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG  
 CTTCAACCACCGCAGTCAAGTGCCCTCCGGGGACAGTCGACGTGTCTATGATGTAACCTGAACCTCAGAGGAAA  
 CAAGAACCCTCCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGCGGACATGTGCGTGAGGAGATTCTCTCT  
 GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAAGTGTACCAGGAGAAGGACGCGCTCCA  
 GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCTGCCCCGAGGCGGTGGACCTCTCGAA  
 CTTCTGTCTGGGCCACCATTTCTCTGTCTCCCCTCTTCAGTTTGTCTTGGGCGTCTTGGCAGCGGATCACC  
 TCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTTCGACACTGATAGGAGATCGCT  
 TGAACCTGGGAGGTGGAGATTGCAGAGAGCTGAGATGGCATCACTGTACTCCAGCTTAGGCACAGAGCAAGACT  
 CAGTCTCAAAAAAAAAAAAAAAAACAAAAAAAAACCCGAGAAATCTGGAGTTGAAGTGTGTAGTTACTGACATGAAA  
 ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT  
 TTTCAAGGCTAATGAAAAAAGATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGCTCACACAAATCAA  
 CATATGCATGATGAGAGTCCCAGAAGGAGAGGAGAGAAAGGTCAGAAAGATGGCCACAAGCTGATGAAAAACA  
 GTAACTACCCACTCAGGAAGCTCAGTGAACCTCCAATGAGGATGAATATCAGAGATCCACACTTAGATATTTTCA  
 AATCAAGTGTCAAATGACAAAGAACTTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTTG  
 ATCAGATTAACAGCTCATTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGATGAACACTGTTGAAGGCAA  
 AACCTTCAACTGTAATTATTGGACTTTTGAGTCTTAGATGGTCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA  
 ATTTAATCCCTAATAACAATTAGTCAAGCTTCCTTGACCTGTAGGAAGGCCGTGCTTTAGGCCGGGCACAGTGGC  
 TTACACCTGTAATCCAGCAGCTTTGGGAGGCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACCTCT  
 GAGTTCAAGTGATCTGCCCGCTCAGCCTCCCAAAGTGTTGTGATTGCAGGCGTGAGCCACTGCGCTGGCCGGA  
 ATTTCTTTTAAAGGTGAATGATGGGGGCCAGGCACGATGGCTCACGCTGTGATCCCAAGTAGCTTGGATTGTA  
 AACATGCACCACCATGCCTGGCTAAATTTTGTATTTTAGTAGAGAGCTGTAGCCAGGCTGGCTCGATCTCCT  
 GACCTCAAGTGACCACCTGCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGCTGCCCTGGCCTGA  
 GCATCTGTGATGTCTATTGGCCATTTGTATATCTTCTATCTTCTTGGGGAATGTCTGTTCAAGTCCCTTG  
 CCTTTTAAATTTTATATTTATTTATTTATTTATTTTATTTGAGACAGGGTCTTGTCTGTGCCCAGGCTGGAGTA  
 CAGTGGCACAGTCTGGCTCACTGCAGCCTCGACCTCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT  
 AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA  
 TGCCCAGGCTGGTCTGAACCTCTGAGCTCAAGTGATCTGCTTGTGAGCTCCCAAAGTGTGGGATTACAGA  
 CATGAGCCACTGCACCTGGCAAACCTCCCAAAATTCACACACACACAAAAAACCTGATTCAAATGGGCA  
 GAGGGGCCGGGTGTGCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG  
 CAGTGAGTCGAGGTTGTGCGACTGCATTCAGCCTGGACAACAGAGTGAGACCTTGTCTC

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**FIGURE 166**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213  
><subunit 1 of 1, 368 aa, 1 stop  
><MW: 42550, pI: 9.11, NX(S/T): 1  
MGLLAFLKTQFVLHLLVGFVSVVSGLVINQVQLCTLALWPVSKQLYRRLNCRSLWSQLV  
MLLEWWSCTECTLFQDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK  
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR  
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK  
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN  
FLSWATILLSPLFSFVLGVFASGSPLILTLFLGVFGAASFGVRRLLIGESLEPGRWRLQ

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169



**FIGURE 167**

GATATTCTTTATTTTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCTCTGGGGCA  
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTGTGGGGTTGGTGGCAGGCAGGCCG  
 GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTATACAAATGGG  
 GATAGCTGGGGTCTGAGACCTGCTTCCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTT  
 TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTGTCTCTTAGGATCAA  
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGT  
 ACATGTGGTGTCTCTTGTCTGTTCCCTG**TAA**TGTGGTATGCCATGGGGTCTTGCACAAGCCT  
 TTCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC  
 ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
 CTTGTTTAATGCTCTCATAAGACCACCTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
 TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCGAGAATGCCAGCTCTGAGC  
 TGGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT  
 CATGTTTtagagactAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
 GATGGTGTAGGGCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
 TGCAGGTCTGATTCAGTAGGCCAGGTTGGGCATCTCTAACAACTCCCAGTGATGCTGA  
 TGCTGGTCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
 TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
 TCAAGACTAGCCTGGCCAACATGGTGAACCCCATCTGTACTAAAAATACACAAATTAGCTG  
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

**FIGURE 168**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHIHLVCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGLRRLIRPWVRR
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
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**Important features of the protein:****Signal peptide:**

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**FIGURE 169**

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCGCCTCAGCCTCCCAAGGTGCTGTGA  
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTTCAGCAACTAAAAAGCCAC  
 AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGTCTTACTCTACCTAC  
 ATTAATACTGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT  
 CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC  
 ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
 ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGA  
 GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGACA**AGCCCCGAAGATTT  
 CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCAT  
 CTAACCTTTTTCATGTCTGACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
 AAGCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
 TATGTGACAGGACTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA  
 GGGGAAGAACTTGTCGCAAATTATGGGTGAGAAAGATGGAGGTGTTGGGTTATCACAGGC  
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGCTGCTG  
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTC  
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
 GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCT  
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA  
 TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG  
 CCAACATTTTGGGAGGCCGAGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG  
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
 GTGTGCCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT  
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
 AAAAAATAAAAAAGAATTATGGTTATTTGTAA

**FIGURE 170**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA

SPCWPLAGAVPSPPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

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**FIGURE 171**

GC GGGCCCGC GAGTCC GAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
CCGCCGCTCCTGCCCCGCGCC**ATG**ACCCAGCCGCTGCCCCGGCTCTCCGTGCCCGCCGCGCT  
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTCCTGGGGAGGCGGT  
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG  
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
CCTGGAGCAGCCGCAGGGGGATCTATGATGACCTGCGAGCAGGCCCAGCTCTTGGCCAACC  
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
CTGGCCCTGGCCCTGGCGCTGCCCCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
GCCCCCGAGCTGGGACGGCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC  
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC  
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC  
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
GACGTGAGGTCTACATCAGCCTCCTGCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
**CTAG**GGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC  
CCTGAGTTTAAATTGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAAA

**FIGURE 172**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282  
><subunit 1 of 1, 262 aa, 1 stop  
><MW: 28809, pI: 8.80, NX(S/T): 1  
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSR  
MREHPALRSRLRLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL  
PADGRVVTCEVDAQPELGRPLWRQAEAEHKIDRLKPALETLDELLAAGEAGTFDVAVVDA  
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRYIS  
LLPLGDGLTLAFKI

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

[illegible][illegible]

**FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD  
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSA PPPVSSSDSEAPEANPADGSDADEDDER  
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE  
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV  
AMARSASSSSSSSSSSSDSDVSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV  
DRISEWKRRDEARRRELEARRRREQEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD  
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAKKSAKKPQSSSTEPARKPGQKEKRV  
RPEEKQQAQKPVKVERTRKRSEGFMSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC  
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEKAAEVYTRLKSRVLGPKIEAV  
QKVNKAGMEKEKAEKLAGEEELAGEEAPQEKAEADKPSTDLSAPVNGEATSQKGESAEDEKEHE  
EGRDSEEGPRCGSSDLHDSVREGPDLDPRPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13



**FIGURE 175**

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA  
 ACACCATTTGAAGAGAACATTTGTTTTCATCATGAATGCTAAATAAGAGATGAAAGACTTAAAGCCAGAAGCCAAAGA  
 TTTTCACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCAGTCACCTGGCATTGGAAGCA  
 AAATATTCCAAGACTCAAGCTAACCTTACAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTTGGGTTTCATC  
 AGAAGGACTGGATTTCAAACCTTTCTCTTTAGATGAGGAAAGAGGCGGCTGCTCTTGGGAGCCAAAGACCACAT  
 CTTTCTACTCAGCTCTGGTTGACTTAAACAAAAATTTTAAAGAAGATTTATTGGCTGCTGCAAGGAACGGGTGGA  
 ATTAGTAAATTAGCTGGGAAGATGCCATCAGAAATGTGCAAAATTTCTCAGACTTTCAGCCCTATAACAA  
 AACTCACATATATGTGTGTGGAACCTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA  
 GGATATTATATTTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCTTTTCGATCCTCAGCAGCC  
 TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTTCTTGGCAAGAGATACTGCATT  
 CACTCGATCCTTGGGCCCTACTCATGACCACCTACATCAGAACTGACATTTTCAGAGCAGTACTGGCTCAATGG  
 AGCAAAATTTTATGGGAGGTTTCTTCATACCAGACCTACAATCCAGATGATGATAAAATATATTTCTCTTTCCG  
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT  
 AGGAGGACCAACGCAGCCTGATAAAGCACTGGAGCAGCTTTTCTTAAAGCCAGACTGATTTGCTCAATTCCTGGAAG  
 TGATGGGGCAGACTACTTACTTTGATGAGTTTCAAGATATTTATTACTCCCCACAAGAGATGAAAGAAATCCTGT  
 AGTATATGAGGCTTTTACTACAAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATGATGCTGCTGACAT  
 CAGAGCAGTTTATTAATGGTCCATATGCTCATAAAGGAAAGTGCAGACCATCTGTGGGTGATGATGAGGGAGAA  
 TCCTTATCCACGGCCCTGGTACATGTCCAAGCAAAACCTATGACCACCTGATTAGTCCACCCGAGATTTTCCAGA  
 TGATGTCATCAGTTTCATAAAGCGGCCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAAGCTT  
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGTGGATCATGTTCATTGCAAGAGATGGCCAGTACGA  
 TGTAAATGTTTCTTGGAACAGACATTTGAACCTGTCTCAAAGTTGTGACGATTTCAAAGGAAAGGTTGGAATATGGA  
 AGAGGTATGCTGGAGAGTTTCTTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGAAGCA  
 GCAACATTTGTACATTTGGTTCCTCCGAGATGGATTAGTTTCACTCTCTTGCACAGATGCGACACTTATGGGAAGC  
 TTGGCGCAGACTGTTGTCTTGCCAGAGACCCTACTGTGCTGGGATGGAATGCATGCTCTGATATGCTCCTAC  
 TCTTAAAGAGGAGAGCTAGAGCCCAAGATGTAATAATATGGCGACCCAAATCACCCAGTGTGGGACATCGAAGACAG  
 CATTAAGTCCATGAACCTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGATATCC  
 TAAATCCCAACAGCAACTATTTAAATGGTATATCCAGAGGTCAGGGGATGAGCATCGAGAGGATTTGAAGCCCGA  
 TGAAGAATCATCAAACGGAATATGGGCTACTGATTGCAAGTTTGCAGAAGAAGGATTTCTGGGATGTTATCTG  
 CAAAGCCCAGGAGCACACTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA  
 AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA  
 CTACATCCAAATCCTTAGCAGCCCAAATCTCAGCCTCGACCAGTACTGCAACAGATGTGGCAGAGGAGAGCG  
 GAGCAGAGAAACAAGGGGGCCCAAAGTGAAGACACATGCAGGAAATGAAGAAAGAACGAAATCGAAGACATCA  
 CAGAGACCTGGATGAGCTCCTTAGAGCTGTAGCCAGCTAGTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC  
 TATAAAACATTTGCCCTTCTGTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGAGTTTGTGAAGG  
 CACAAGACATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAATTCATTGTAACAGGTTT  
 CCAAGAACAAATCTTGACACAAGCAAGTATAAGAAATATCCTTAAATATAGGGGTTTACAGTTGTAATGTTTAA  
 TGTTTTGAAGTTTGAATTTATTGTCTGATGTAATAGTTGAGCTAAGCAAGCCCGAATTTGATAGTGATAAGGT  
 GCTTTATTCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAAGTTGTGCTATGTTCTTATGAACAGATATAT  
 CATTCCTATTGAGAACCAGCTACCTTGTGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCCATATC  
 AACAGGAACCTTCTCAGTGAGCCATTCACTCCTGGGAATGGTATAGGAATTTGGAGAGGTGCATTTATTTCTTTC  
 TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTTGATTTACTGAAGGCCTAATGTTTCCCCAGGATTTCT  
 ATTGACTAGTCAGGAGTAACAGGTTTCAAGAGAGAAGTTGGTGCTTAGTTATGTTTGTATGAGTATATACTAA  
 GCTCTACAGGGACAGATGCTTAATAATACCTTTAAATAAGATATGGGAAATATTTTAATAAACAAGGAAACAA  
 TAATGATGTAAATGCATGCTGATGGGAAGGCATGAGATGGGATTTGTAGAAGACAGAAGGAAAGACGCCAT  
 AAATTTCTGGCTTTGGGGAAACCTCATATCCCATGAAAGGAAGAACAAATCACAATAAAGTGAGAGTAAATGTAA  
 TGGAGCTCTTTTCACTAGGGTATAAGTAGTGCCTTGTGAATTCATCTGTGTTAAAAATCTAGATATAACA  
 AACTGCTCTAGCAAAATCTGAGGAACATAAATTTCTTGAAGAATCATAGGAAGAGTAGACATTTTATTATAACC  
 AATGATATTTTCATATATATTTCTCTCTTTTAAAAATATTTATCATACTCTGTATATTTCTTTTACTGTC  
 CTTTATTCTCCTGCTGATTTGGATTTTGTGATTATTTGAGTGAATAGGAGAAACATATATAACACAGAGA  
 GAATTAAGAAAATGCAATTTCTGGGAGTGGGGATATATTTGTTGAATACAGAACGAGTGTAATAATTTTAAAC  
 AACGGAAGAGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAAT  
 GTAGTATTGTTTTTGTAAATTTAAACAATAAAGCCTGCTACATGT

**FIGURE 176**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL  
 GSSEGLDFQTL LLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA  
 NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDI IFKLDTHNLESGRLKCPFD  
 PQQPFASVMTDEYLYSGTASDFLGKDTAFT RSLGPTHDHHYI RTDISEHYWLN GAKFIGTFF  
 IPDTYNPDDDKIYFFFRESSQEGSTSDKTI LSRVGRVCKNDVGGQRSLINKWTTFLKARLIC  
 SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP  
 YAHKESADHRWVQYDGRIPYPRPGT CPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV  
 AGGPTL FKRINVDYRLTQIVVDH VIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVLEE  
 LQIFKHSSII LNMELSLKQQQLYIGSRDGLVQLSLHRCDTYKACACDCCLARDPYCAWDGNA  
 CSRYAPT SKRRARRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA  
 TIKWYIQRSGDEHREELKPDERI IKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTLN  
 VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN  
 KGGPKWKHMQEMKKKRNRRHRDLDELPRAVAT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

**FIGURE 177**

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGACAGGTCATCCTGGAGCATGCCACCCGCGGGAGCAGA  
 CAACCTCCCAGGTAACTGGGAGCAAGACCTGAAGCTGTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC  
 CTCAGCAGTTTCAGCCAGCAGGACTGATCAGGTGTGTGTCTTGGAGTGGGAGCAGAAGCGGTGGCTGGCAGA  
 GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAAGCCGAGCTGCCGTGACTACAAAGTCCAGAACCCTGGGCATC  
 GGGTGAGGTGGGGGGCACAGGTGTCTATGTGACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG  
 AGCCATTGAGGTGTCTATGAGACTACAGAGGGGAGGGAAGGTATTTAAGGTACAGGTGGGCACAATAGTTAA  
 GAGCACAATTTTTGGAGCTAGACCGACATAGGTTCAAATTTCTTCTGTGTCTTCTGTGCTCTCTGAGGCCAGGT  
 AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCTAAAGTAGGGCCAATAATAGCACCACCTCAT  
 AGGGAAGATTAAATGACATAATGTATGTATGATGCACTAGCAAAGTACCACTCCCATAGTAAGTCATGCCCCACAG  
 TATTTCCACCCACCCCTGTTCTCTGCTTCCCAACAGGTAAGTGAACGACTGGAGCAGAGCGGCAGCAGGCTT  
 CAGAGCGGGAGGCTCCAAGCATAGAACAGGTTACAGGAAGTGCAGAGAGACTCCGCCGGGCACAGGTGAGCC  
 AGGTGAAGGGGCTCCAGGCTGAGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGGCTGCTGCCAGGCCAGCC  
 TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGTCCAGAGGACCTCTCTC  
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCCC  
 CCCAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACCTGGTATTTCCGCTACAGGACGGCGTGAGGATG  
 AGCTGACAATCAGGAGGTGAGTGGCTGGAGGTCTATAGAGGGGAGAGTGTGACCAATGGGTCAAGGCTCGGA  
 ACCAGCAGCGGCAGGTAGGCTTTGTCCTTGGCGATATCTCAACTCCCGACCTCTCCCTCCAGAGCAGGCC  
 AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCTTGGCACAGGCCCTGTACAGCTACACCGACAGA  
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGCACTCATCGTCTGCTGCCCGGGCCCAAGATGGAGTAGATGAGC  
 GCTTCTGGAGGGGAGAATTTGGGGCCCTGTTGGGGTCTTCCCTCCCTGCTGGTGAAGAGCTGCTTGGCCCC  
 CAGGGCCACCTGAATCTCTGACCTTGAACAGATGCTGCCGTCCCTTCTCTCCACAGCTTCTCCCCACCTGAC  
 CTACCTCTGTGTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAGAGCCCTGGACTTCCCTGGGTCTCTGG  
 ACATGATGGCACCTGACTCAGGCCGATGCGTCCACCCTCCCGCCGGCTAAAGCCCGGATCTTGGCCACC  
 CAGATCCCTCACCCTGAGGCGCAGGGAAGCCTTGACCCCAAGTGATGCTGCTGCCCTATCTCAAGCTGTGAGA  
 CCACACCATCAATGATCCAGAGCAACACAGGCCAAAAGCTGGAATCGCCCTTATTTCCACCTCAGCTCCAAGGT  
 GGAACCTGACCTTCCCTTTCTAGAGCTGGAACCCACTCCTTTTTTCCCATTTGTTCTATCATCTCTAGGACC  
 GGAACCTACTCCCTTCTCTGTCTAGACCTATCTAGGGTGGTGAATGCTGAAATCTCTGGGGCTGGAACCC  
 ATCCATCAAGGTCTCTAGTAGTTCTGCCCCACTCTTTCCCACTCCCTGGTCCATGACCCACCCACTCTGGATG  
 CCAGGTCCTGAGGCTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
 CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGCCACGAAGGCCAGGCCAGGGCTGGGCTCTGTG  
 CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACCAAGGGCAGGGGCTGCTCCAGCTGCCAC  
 GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCCGGGGCAGGCAGCTGTGTCAGAGGGGAGAAGAGAGAC  
 TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC  
 AGCTGGGGGCGAGTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCAACCCCTGGCCCTGCCAGCTGGTAG  
 TCCATCAGCAACAATGAAGGAGACTTGGAGAGGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCAGC  
 TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCCAAACCAAGGATTATAGCAAGGCTAAGCCTGC  
 AGTTTACTCTGGGGGTTGAGGAGCCGAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA  
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACCTTGAGAGAAAGGGGAGGG  
 TCAACAATGAGAGACCAGGAGTAGTCTTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCAGGCCAGTGC  
 AGTCCCGGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGTTTGTCTGGCTGCCATTTGCTCTTGTAGTGG  
 GCAGCCCTGGGCTTGGGCCCTCCCTCCGGCCCTCAGTGTGGCTCTGCAGAGCTCTGGGGTTCCTTCAAGT  
 CACGAGGGGTAGGCTGCTGTCCTGAGTCTCCATTCTGACTGGGGGCTGGCTAGGACTGGGGCTGTGGCC  
 TCTCAGGGGCGAGCCTCTCATGGCAGGACTCCCTGCTTGGGCTGCCCTCCCCAGAGCCCTGACCAACCCCTG  
 GGTCTGTGTCACCCAGCAGGCCCACTCTGCTGTGGGGAGCCATCAGGTGTTCTGTGAGTCCATGAGGCT  
 TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGTTTATAGACCAACTCAGAGGCTGGTGTG  
 GCCCTCCCTCTGACCAAGGACATCTGAGTTTGGTGGCTACTTCCCTCTGGCTCAAGTAGGGGAGGCTTCTC  
 AGATTGTGGGGCAATTGTGTAGCTCACTCTGCTGGAGCTCCAGTCCAGGAGAAAGGAGCCAAAGGCCACTT  
 TGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACTTGCCTCCCTGCCCC  
 CAGAGAACACAGTGGTCTCCCTGCTCCGGGGCGGCTTTTCTCTCTGGAGGCTCCCTGACGGACAAGTGGAG  
 GCCTCTGTGTCGGCTGCAATGATGCAAGGGGCTGCAGAGCCAGGTCAGTGTGATGATGGGAGGGGCTC  
 CGTCTGCAAGCTGGAGGTGGCATCCACTGGACAGCAGGAGGAGGGAGTGAAGTTTCAATTTCCATTTCCCT  
 TCATGTTTTGTTTCTTACGTTCTTTCAGCATGCTCCTTAAACCCCAAGAGCCCAATTTCCCAAGCCCCATT  
 TTTCTGTCTTATCTAATAAATCAATATTAAAG

**FIGURE 178**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTFVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA  
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPATAEDALS  
DFEECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW  
VKARNQHGEVGFVPERYLNFPDLSPSSQDSDNPCGAEPTAFLAQALYSYTGQSAEELSFP  
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPPSLLVEELLGPPGPPPELSDPEQMLPSPSPSS  
FSPAPTSVLDGPPAPVLPDGKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT

**FIGURE 179A**

CACAGGGAGACCCACAGACACATATGCACGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA  
 GAAGGCAGAGACAGGGCAGGCACAGAGAGGCGCCAGACAGAGTCCACAGAGGAGAGGCCAGAGAACTGCAGA  
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCACAGCCCTGG  
 GCACCTCTCCCAAGCCCAGGACTAAGTTTCTCCATTTCCTTTAACGGTCCCTCAGCCCTTCTGAAAATTTGGCC  
 TCTGACCTTTGGCAGGCTCCAGGCCCTAGGCTACAGAGAGGAGTTCCTCAAAGCTCGAGGGCTGACAGTGCAGTA  
 GCCCTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAGTGCCTATGTCCTCCAGACAGAGCTCGCATCCCGGGAGGGG  
 CTTGGCAGGGCGCTGGCTGTGGGAGGCCAACCTGCCTCCTGCTCCCATTTGTCGCTCTCTGGCTGGTGTG  
 GCTGCTTCTGCTACTGCTGGCCTCTCTCTGCCCCAGCCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGAGAT  
 CGTGTTCACAGAGAAGCTCAACGGCAGCGTCTGCTGGCTCGGGCGCCCTGCCAGGCTGTTGTGCCCTTGCA  
 GGCCCTTTGGGAGAGCGTGTCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGCTGACAGTGCAGTA  
 CCTGGGCCAGGCGCTGAGCTGCTGGGTGGACGAGGCTGGCACCTACCTGACTGGCACCATTCAATGGAGATCC  
 GGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTACAATATCGGGGGGCTGAACCTCCA  
 CCTCCAGCCCTGGAGGGAGGCACCCCTAATCTGCTGGGGACCTGGGGCTCACATCTCAAGCCGGAAGAGTCC  
 TGCCAGCGGTCAAGTCCCATTGTCAACGCTCAAGGCTCCTCTTGGAAAGCCCCAGCCCCAGACCCGAAGAGCCAA  
 GCGCTTTGCTTCACTGATGATAGATTGTGTGAGACACTGGTGGTGGCAGATGACAGATGGCCGCTTCCACGGTGC  
 GGGGCTTAAAGCGCTACCTGCTAACAGCTGATGGCAGCAGAGCCAAAGCCCTTCAAGCACCAGGATCCGCAATCC  
 TGTGAGCTTGGTGGTGACTCGGCTAGTGAATCTGGGTCAGGCGAGGAGGGGCCAAGTGGGGCCAGCTGCTGC  
 CCAGACCTGCGCAGCTTCTGTGCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACCTTTGA  
 CACAGCCATTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGG  
 CACCGTCTGTGACCCGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAAGCTTCACTGCTGCTCA  
 TGAATCGGGTCACTGCTTCAACACTGCTCCATGACAACCTCAAGCCATGATCAGTTTGAATGGGCCCTTTGAGC  
 CTGCTCCTGCTCATGTGGCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGTTCCCTCGAGTCCGCGCCTT  
 CATCACTGACTTCTCGGCAATGGCTATGGGCACTGTCTTGTAGACAAACAGAGGCTCCATTGCATCTGCTGT  
 GACTTTCCTGGCAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCGACTCACGCCATTGTCTC  
 ACAGCTGCCCGCCGCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAACA  
 CTCGCCCTGGGCCCATGGCACCCTGCGGCCCGGCACAGGCGCTGCATGGTGTGCTGCTGCCATCCATGGACCA  
 GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCCCTTGGGGACCTGAGTGGTCACTGCTCCTGGACCTG  
 TGGGGGTGGTGTCCAGTTCTCTCCGAGACTGACAGAGGCTGTCCCCGGAAATGGTGGCAAGTATGTGAGGG  
 CCGCGTACCCGCTTCGCTCCTGCAACACTGAGGACTGCCAATGGCTGACCTTCACTTCCCGGAGGAGCA  
 GTGTGCTGCTCAACCCAGCCGACGCTTCAAGAGCTTCCAGGGCCCATGGACTGGGTTCCTCGCTACAC  
 AGGCGTGGCCCCCAGGACCCAGTGCAACTCACTGCCAGGCCCGGCACTGGGCTACTACTATGTGCTGGAGCC  
 ACGGGTGGTATGAGGGACCCCTGTTCCCGGACAGCTCCTCGGTCTGTGTCAAGGCCCATGCATGCATGCTGG  
 CTGTGATCGCATCATGGCTCCAAGAAGAGTTTGACAAGTGCATGTTGTGCGGAGGGGACGGTCTCTGTTGTCAG  
 CAAGCAGTCAAGGCTCCTTCAGGAAATTCAGGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGCCACCCA  
 CATTCTTGTCCGGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA  
 TGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGGAGTCAGCTTGGCGTA  
 CAGCGGGCCACTGCAGCCTCAGAGAACTGTCAAGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTCT  
 AGTGGCTGGCAACCCCGAGGACACAGCCTCCGATACAGCTTCTGCTGCCCGGGCGACCCCTTCAACGGCCAG  
 CCCCCTCCCGAGGACTGGCTGCACCGAAGGACACAGATTCTGGAGATCCTTCGCGCGCGCCCTGGCGGGCAG  
 GAAATTAACCTCACTATCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTACCTGGGAGAAAGAGAGAGCTT  
 CTGTTGCTGCCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGCGTGAGAGCTGCCCTCCTCTGCTCCCTAAT  
 GCGCAGGCTGGCCCTGCCCTGGTTCCTGCCCTGGGAGGCACTGATGGGTATGTGGATGGAAGGGCTGACAGAC  
 AGCCCTCCATCTAAACTGCCCTCTGCCCTGCGGGTCAAGGAGGGAGGGGAGGAGGAGGGGCTGGGCGCT  
 CAGTGTGATTTATTAGTATTTATTACCTTTTATTAGCACCAGGGAAGGGGACAGGACTAGGGTCTCTGGGAA  
 CCTGACCCCTGACCCTCATAGCCTTCACTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATATAGTATAGTGTG  
 TGTGATGCGTGTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATGAGGTACAACTGTTCTGCTTTCCCT  
 TCTCGTAATTTTATTTTTGGGAAAGAAAGTCAAGGGTAGGGTGGGCTTCAAGGAGTGAAGGATGATCTTTT  
 TTTTTTTTTCTTTCTTTCTTTCTTTTGTGAGACAGAATCTCGCTCTGTGCCCGAGGCTGGAGTGAATG  
 GCACAACTCGGCTCACTGCCTCTCCGCTTCAAGTGATTTCTCATGCTCCTGAGTATCTGAGTATGCTG  
 GGATTACAGGCTCTGCCACCACGCCAGCTAATTTTGTGTTTGTGTTGAGAGACAGATCTCGCTATTGTC  
 ACCAGGGCTGGAATGATTTCAGCTCACTGCAACCTTCGCCACCTGGGTCCAGCAATCTCCTGCTCAGGCTCC  
 CGAGTAGCTGAGATTATAGGCACCTACCACACGCCCGCTAATTTTGTATTTTAGTAGAGACGGGTTTAC  
 CATGTTGGCCAGGCTGGTCTCAACTCTGTGACCTTAGGTGATCCACTCGGCTCATCTCCCAAGTGTCTGGGAT  
 ACAGGCTGAGGACCCGCTGCTGGCCACGCCCAACTAATTTTGTATTTTTAGTAGAGACAGGTTTCAACATG  
 TGGCCAGGCTGCTCTTGAATCCTGACCTCAGGTAATCGACCTGCTCGGCTCCCAAGTGTGGGATTACAGG  
 TGTGAGCCACACGCCCGGTACATATTTTAAATGAATCTACTATTATGTGATCCTTTTGGAGTCAGACAG

**FIGURE 179B**

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTGCCAATAATAATACCTCCCTTAGAAG  
TTTGTCTGTGAGGATTAATAATGTAATAAAGAACTAGCATAACTCAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAGGAAA

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**FIGURE 180**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPIPREEEIV  
FPEKLNQSVLPVPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPPELLGGAEP  
GTYLTGTINGDPESVASLHWDGGALLGLVLQYRGAEHLQPLEGGTPNSAGGPGAHILRRKSP  
ASGQGPNCNVKAPLGSFSPRPRRAKRFAFLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA  
AAKAFKHPISIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLSRFCAWQRLNTPEDSGPDHF  
DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD  
NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL  
PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCCALWCSCGHLNNGHAMCQTKHSPWADGTPCG  
PAQACMGGRCCLHMDQLQDFNIPOAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRVPVPRNGGKY  
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVPQDQCK  
LTCQARALGYVYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG  
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGNPGRHSIYLALKLPDGSYALNGEYTL  
MPSPTDVVLPGAVSLRYSGATAAETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT  
PSTPRPTPDWLHRRRAQILEILRRRPWAGRK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG  
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
 AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT  
 AATTGTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAATTTGATCCTGTG  
 ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
 TTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
 TTTTCTTAAAAATTCCAAAATTTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTTACTG  
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
 CTGCTACCAAGGAGGACGAGTCATCTGTCTGTGCATCATGCCTTGTAAGTGGTGGGTGGCCC  
 GCATGCTGGGGAGGGTCTAATAGGAGGTTTGAAGCTCAAATGCTTAAACTGCTGGCAACATAT  
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT  
 CTCAGAAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
 AAAAAAAAAAAAAAAAAA



**FIGURE 182**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLNSKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLDERGYCCIIYCRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGGCCAGGGAGCTGCC  
 CGGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
 GCTCAGCTTCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
 GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
 ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA  
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
 GGCACCCTGCTTTGCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCGCC  
 CAGGGCCACCACGACCACTGCAAAACCCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
TGAGTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
 AATGGAGGCAGGGGTTCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATTATATATAT  
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

**FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
 QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTFAKTTFAILGGTL  
 FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLCLSCQ  
 DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

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**FIGURE 185**

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATGT**TCCACCACCACATGCCAAGTGGTGGCGTTCTCT  
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC  
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
 GTGAGGCAGAGTTACAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC  
 CATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC  
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
 AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
 GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
 GCATGGGTGGGATGGTGCAGACTGTTTACAGCCAGGTACACATTTGGTGCGGCTCTGTTCGTG  
 GGCTGGGTGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
 CCTGGCACCAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTG  
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG  
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTACCCAAAA  
 AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC  
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTC  
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC  
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA  
 TTTCCAGCTTATCCCCAAGAAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT  
 CTGCTGTTTGAATTTTGCTCTCCCAACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA  
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
 TGATCTTAAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTG  
 CTGTTGACATCTTCTTATTACAGCAACACCATTTCTAGGAGTTTCTGAGCTCTCCACTGGAG  
 TCCTCTTTCTGTGCGGGGTGAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT  
 TTAAGTCCTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA  
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT  
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATCCATGAAAAGCTCACACCTGTAATC  
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG  
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG  
 GCATACACCTGTAGTCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG  
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAA  
 ACTAATTCCTTAA

**FIGURE 186**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTE  
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM  
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTQTRYTFGAALFVGWVAGGLTL  
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE  
DEVQSYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

**FIGURE 187**

GGAAAACTGTTCTCTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG  
 GAGTCCAGCTGGCTAAACTCATCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG  
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGG  
 AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG  
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGTCTGG  
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCTTTC  
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA  
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT  
 GTTGCCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT  
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA  
 GATACTCGATACCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG  
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTGTGTATGTTTTTTTAACTTTACTATAAAGC  
 CATGCAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTTA  
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA  
 GCTATTTTCAGCAGAATGAGATATTAAACCCAAATGCTTTGATTGTTCTAGAAAGTATAGTAAT  
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT  
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
 TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG  
 TCCATTACACTGAATAAATAGAAGTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG  
 AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTATAATGA  
 AGATTAATGAAGGCTTAATCAGCATTGTAAAGGAAATGAATGGCTTCTGATATGCTG  
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTCTTTATCCTCTTCTCCAGAGGCTTTTTTT  
 TTCTTGTGTATTAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA  
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
 GTTTTAGGAAAGTGAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA  
 GAAATCATATATGTATGGATATATTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
 AATATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTCATTTGCTTACCAAAAAACAACA  
 ACAAAAAAGTTGTCCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAATTTG  
 TCATTTTTGTCTGTGAAAAATAAATTTCTTCTGTACCATTTCTGTTTAGTTTTACTAAA  
 ATCTGTAAATACTGTATTTTTCTGTTTATCCAAATTTGATGAACTGACAATCCAATTTGA  
 AAGTTTGTGTCGACGTCTGTCTAGCTAAATGAATGTGTTCTATTGCTTTATACATTTATA  
 TTAATAAATTGTACATTTTTCTAATT

**FIGURE 188**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRM  
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI  
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF  
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

**FIGURE 189**

TCGCCATGCCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTTCATCGGCAACAGCAT  
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTCATCGCCCTCCTTGTGGCCCTGTTGCGCTTGCTGGTCTACCTTGTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCTGGTGCTCACCTCTGGGA  
TTGTCTTTGTCTATCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGTTGCTGTGCTGCACTT  
GCCCCTCGGGGGGGTCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCCT  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTGGACGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT  
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTTCTTTGACTGAGGATATTTAAATTCATTT  
GAAAAGTGAAGCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTGG  
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCATCTTAGAAGC  
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCTCCAAAGAGTTCCTGCTGCTGCTGGGGCTGGGCTTCCTTAGATGTCACTGGACAGCTG  
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCCCTCCGTCTGATAAGACG  
TCCACCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCTCGTCTACCCCTTTACACTCACATTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA



**FIGURE 190**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM  
QCKVYDSELLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV  
FVISGVLTLLIPVCWTAHAIIIRDFYNPLVAEAQKREL GASLYLGWAASGLLLLGGGLLCCTCP  
SGGSQGPPSHYMARYSTSAPAIRGPSEYPTKNYV

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

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**FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTG  
 AGCATCTTCTACCACTCCGAATTGAACCACTCTTCAAAGTAAAGGCAATGGCATTCTTATCCC  
 TTGCCAATTGCTGGGCTGGTTCTTGGGTTCCCTGGCATGGTGGGGACTCTTGCCACAACCCT  
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
 TGGGAAGGGCTCTGGAATGCAATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
 TAGCTCCTTGTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG  
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
 GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCTCTTCATCCTGAC  
 GGGTATCTTCGTTCTGATTCGGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
 ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
 AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTCTGCTGCAACAGAAA  
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
 ATACGACAATGCTTAGTAAGACCTCCACAGTTATGTCATAATGCCTCCTTTTGGCTCCAAGT  
 ATGGACTATGGTCAATGTTTTTTATAAAGTCTGCTAGAACTGTAAGTATGTGAGGCAGGA  
 GAAGTGTCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG  
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
 GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

**FIGURE 192**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER  
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL  
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV

**Important features of the protein:**

**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATGA**AGATCACTGGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
CATACCTACCAGTTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCA**CTT**GTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCT**TAA**ATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCAGGCTCTGACTG  
AGTTTCTTTAGTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG  
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA

### FIGURE 194

**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCTTGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAACTAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCT  
CTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT  
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

**FIGURE 196**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFL  
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEYYGDIYQRHYD  
EDSAIGPRSPYGFRHGASVNYDDY

**Signal peptide:**

amino acids 1-30



**FIGURE 197**

CGGCTCGAGCCCGCCCGGAAGTGCCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC  
 GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC  
 CGTCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA  
 CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCCAGC  
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCGACCT  
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTTACAGCAACACCGCCAG  
 CCCCAGACTCCCCGAGGAGCCCTCGTGCTACGGCTGAAATTCCTCAATGATTGAGAGCAG  
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGCCG  
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCTGG  
 GCAGCCTTACCTCCCTCCCAACTGCGTTCTCCTACTGCCACGTGTCCACGAGAGTCGGTCCC  
 CCAAATCCCCCTGCCCCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT  
 GCTGCTGCCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
 CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACCCCTGCTCCTCAGTCTCCTG  
 GCCTTTGCCATGTACCGCCCGTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCTCC  
 GGACCTTGCTCCCCGCGCGCGGGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG  
 CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGCAGAGGACTCCCGGGACTGGCGGAGG  
 CCCC GCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCGCA  
 CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTGCTGCCTCGGCCCGGGGCAGAGCCG  
 GGCCGCCCGGGGGCCCGTCTTAGTGTTCTGCCGAGGACCCAGCCGCCTCCAATCCCTGAC  
 AGTCCTTGGGCTGAGTTGGGACGCCAGGTGCGTGGGAGCTGGTGAAGGGGAGCGGGGAG  
 GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAA  
 AAAAAAA



**FIGURE 198**

MTLIEGVGDEVTVLFSLVLA~~CL~~LLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSFQEPLVLR~~LK~~FLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCFFPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPF~~F~~PLTATLGLAGFTLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

**FIGURE 199**

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC  
TCAGCTGCACCTCCTCCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC  
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT  
GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG  
AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC  
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA  
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA  
TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTCAGGCCGG  
CCTCTCTCTACTGGCTGACAGGATGCCGCCCTGAGATGGAACAGGGTGCGGGTGACCCGTGG  
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTTCTTCTTCTACTGCCTCCA  
CTTCATGTTATTTTCTTCCCTTCCCATTTCACAACTAAACTGACCAGAGCCCCAGGAATAAA  
TGGTTTTCTTGCTTCCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT  
TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

**FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLI SRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI  
NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHC AKRIVSGARGMN  
NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18



**FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCTAGCCCTGCTTGACTGAGAACCCA  
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG  
 CAGAAATGGAATCATATTATTTTTTCCCAAGGAGAAAAACCGGGGTAAAGGGAGGGAAGCAATTC  
 AATTTGAAGTCCCTGTGAATGGGCTTTTCTGAGAGGCAATTAAGAAATCCACTCAGAGAGGAC  
 TTGGGGTGAAACTTTGGGTCTGTGGTTTTCTGATTGTAAAGTGAAGCAGGTCTTGCACACGC  
 TGTGGCAAATGTCTGAGGACAGGTAAAGTACTGGCAGAAAACTTCCAGGTGGAACAAGCA  
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC  
 CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG  
 CAGACTCCAGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCTCTGATGATGGTGGCGATGT  
 TGCACCCCTCCCACCACACCCCTGCACCAGACTGTCTACAGCCCAAGCCAGCAAGCACAGCCCT  
 GAAGCCAGGTACCGCCTGGACTTTGGGGAAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA  
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC  
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGGAAGCAAGGAGCCAGGGCAGGAGAGGTGGG  
 AGCTACCGCCTCATCAAGCAGCCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG  
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTTCAAGCCTGGACCCAC  
 GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG  
 CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCCTCATCTCTG  
 TTTCCATGATGAGGCGCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACAGCATGTC  
 CCAGGCGCTTCTGGAAGGAGATCATCTCTGTTGACGACCTCAGCCAGCAAGGACAACCTCAAG  
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG  
 GCTGGGTGCCATCAGGGCCCCGATGTCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
 TCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT  
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA  
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC  
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG  
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
 TCTTATGTGCTGCGAGGTGGTGAACCTCGAACTGTCTTTCAAGGCGCTGGCTCTGTGGTG  
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCTCAT  
 TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTGCGATTGCTGAGACCTGGCTGGG  
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA  
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTTGTCGGACATTCCACTGG  
 TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA  
 GCTCCACAACACTGGACTTGGCTCTGTGTCAGACTGCCAGGCAGAAAGGGGACATCTGGGGCT  
 TCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
 AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTCAAGCAGGAGCAGGT  
 GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG  
 AGAATGGGATGATTGTCCACATTTCTTCTGGGAAATGCATGGAAGCTGTGGTGCAGAAAGAAC  
 AATAAGATTGTACCTCGTCCGTGATGAGAAAGCCCGCCAGCAGTGGCGATTGGACCA  
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAAGGAAAAGAGAATTTTGGCCATC  
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTATGAAGCTGATCCTTTTGTGT  
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAGAATATAGGAAGTTTCTCCTTT  
 TCACACCTTATTTTCAATTGACTGCTGGCTGCTTA

**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR  
RQDKEAPKRDWGADEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR  
LEGVKLLRSNKR LGAIRARMLGATRATGDVLFMDAHCECHPGWLEPLLSRIAGDRSRVVSF  
VIDVIDWKTQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDSSHSPLDQEATL  
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPCMERLQLQRRLLGCRTFHWFLANVYPEL  
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP  
QHLCFAVRQEQVILQNCTEEGLAIHQHWDQFQENGMIVHILSGKCM EAVVQENNKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTCACAGCTGAGGAAGACCTCAGAC**ATGGA**  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC  
 TGCCCTCCCAACCGCTGCTCAGGGCTCTTCATCCTCCCCTCGAACCCCAACGAGCCAGCC  
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCACGTCATGTGTGCGTGTGGGAGCGAGC  
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCTGCTGCGCACTG  
 CACCCCAAGCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT  
 ATCGTGTGGGGTCCCAACCGTGTCTCGAGAGGATGGAGGGGACCCCACTCTGCCAATCCCGG  
 ATTTCTGGACTATGTTTTTGCAGCCCTCATGGGCTCGCAACCCCAACCCCACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCTGCGGCCATTG  
 CTGTTCGGGGGCGGTGGGAAGGTGTGGACCCCACTCTATGTCAACAATTACCATCTCCAT  
 CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
 GACGAGACCCCTCAGGCGAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCCACTGACA  
 GACCTGTCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCAACCC  
 TGACCATGAGGAGCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CCTTCCAGTTGAACCGG**TGAG**GGGAGGGGCAATGGGATGGGAGGGCAAGAGGGGAAGGCAAC  
 TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGCGTGGC  
 CTCCACAGCCCTGGCCCTCCCAAGGGGGCTGGACAGCTCCTCTCTGGGAGGCACCCCTC  
 CTTCTCCAGTCTCTCAGGATCTGTGTCTTATTCTCTGCTGCCCATAACTCCAACCTGCCC  
 TCTTTGGTTTTTTCTCATGCCACCTTGCTAAGACAACCTGCCCCTCTTAACCTTGATTCCC  
 CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGGTTCTGACTGTGCCCTT  
 TCCCTCTTCCCTCTCAGGATTCCCCTGGTGAATCTGTGATGCCCCAATGTGGGGTGCAGCC  
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA  
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCCCTGCACACCACCGGAACACTCCCCAGCC  
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCTTGTGCACTCACATGAAAGCCTTGCACACTCACTCCACCTTAC  
 AGGCCATTTGCACACGCTCCTGCACCCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCACATTCTGTGCTCAGTCACTCAG  
 TGGTCAGCGTTTCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCTGATGTTTGTTGGTGG  
 TGTGCGCGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGAGCCCTGC  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTATGG  
 TCTCGTCCCATTCCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTACCCCCAGCCCA  
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA  
 AGGGACTCCCATTTGCCCTTCCCTTCTCCTACAGTCCCTTTTGTCTGTCTGTCTGTCTGCTG  
 TCTGTGTGTGCACTTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCTCCCTTCCAGCCT  
 CCGTTTGGGCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC  
 ATCGGGAGCTCTGCCTCCAAGTCTACCTTCCCTTCCCGGACTCCCTCTGTCCCTCCTTT  
 CTTCCCTCCTTCCCTTCCCTCTCCTTTCTCCTTTTCTCCTTCCCTGCTTCCCTCCTCAGGTT  
 CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCCCTTCCCTTCTTCCCTGGCTCCTAGGCT  
 GTGATATATATTTTTGTATTATCTCTTCTTCTTGTGGTGATCATCTTGAATTACTGTG  
 GGATGAAGTTTCAAAATTTCAAATAAAGCCTTTGCAAGATAA

**FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV  
 PGRDGSPGANVIPGTPGIPGRDGFKEGKECLRESFEESWTFPNYKQCSWSSLNYGIDLGKIA  
 ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEN  
 STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

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GTTAACCAGCGCAGTCTCTCCGTGCGTCCCGCCCGCGCTGCCCTCACTCCCGGCCAGG**ATG**G  
CATCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAGGCCCGTGAGAGACCAAGCCCGGCCGGGAGCCCGTGGAACACCGGTCCCC  
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA  
GGGGCCGCGCCCGGCCGCGCGCGACTCGGCAAAAAAAAAAAAAAAAAA

[illegible]



**FIGURE 206**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398  
><subunit 1 of 1, 121 aa, 1 stop  
><MW: 12073, pI: 4.11, NX(S/T): 0  
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTG  
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTGGTGC GCGGCTGAAGGGTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG  
 CGGGCCGGGACGGGC **ATG**GCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA  
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
 ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGT CAGGGGCGCTGCTCACCGACTGGAGC  
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA  
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
 CCGGTTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC **TAA**GTAGCCC  
 CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
 GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT  
 CGACTGT CAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG  
 ACTCGCACGTCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
 GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGGCTCCCCGCCTTCCAC  
 CTGGCTGT CATCGGGTAGGGCGGGGCCGTGGGTT CAGGGGCGCACC ACTTCCAAGCCTGTGT  
 CCCACAGGTCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC  
 TGGCACAAGTAAGTCCCCCTCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
 GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA  
 GGAGGTGGAACCTCAACCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG  
 GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCTTAAAGGTCCCCATAGGGTCTGGTTCC  
 ACCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
 ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC  
 CCTGACCTGGACTTCAGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGCTAGGGGTCCTCT  
 AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
 CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG  
 CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA  
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC  
 ACGAGGGTGTCTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT  
 GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT  
 TGGAAGATGCTGCTGAGTGTCTAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC  
 GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC  
 CTCAGGACCCCCCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGCGGGAGG  
 GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA  
 TGTGATTAAAGTCCCTGATGTTTCTC

**FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK

ELHLAIPAKITREKLDQVATAVYQMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER

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**FIGURE 209**

AGCAGGAGCAGGAGAGGGACAATGGAAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT  
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG  
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC  
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA  
 TAGCATGGTGCAAAAATTTCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA  
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTGCCTGGTAGACAATGAACAACCTG  
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
 CAACAGCCTCCACATGGTGACAGAGTACAACCTGTGACTGTGATTGGGTTATTCAACAGCG  
 TAATTCAGATTTCATCTCTCTCTGATAATGAACAAGGCCCCCCAGAGTATGAAGAGAACATG  
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAATAAAGGAGTCTCAACTGCCAG  
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC  
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGAAAATTGTTGAAAGAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTTGACTTCTCTTGGAACTACATATGGCC  
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACTCAAATCTCAGAGACACTAAACAACAG  
 GATCACTAGGCCTGCCAACACACACACACGACGTCACACACGACGACGCGTGCACAC  
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC  
 TTCTTCTTCTTTTAAATTTTCATATCTCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT  
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT  
 TTGTATACTGCACATGACTTACACACAACATAGTTCTTGCTCTTTTAAAGTTACCTAAGGGT  
 TGAAACTCTACCTTCTTTTATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAGG  
 ATGGTTTTTAAACACCTTTGTGAAATTGTCTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAAATAGACCATGTGAAACTCCATGCTTGGTTAGCATCTCCAACCTCCC  
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

**FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDPAAAMEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVEHVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

**FIGURE 211**

GGAGAGCCGCGGCTGGGACCGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGGCGCGGGTG  
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATGG**CAGCGTCCGCCGGAGCCGGG  
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGCTGGCGGCGGCGCTTGG  
 GCTCTTGACAGCTGGAGTATCAGCCTTGGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC  
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTC  
 CCAAGGGCAAGTGTAACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG  
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC  
 TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
 TGTCTGAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
 CTGTGGTCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA  
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC  
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTGTAAAGAGTCTGCCTTCTGGATCTCACC  
 AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC  
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC  
 CTCAGCAAGAAAACAAACAACTGGACTCTCGTGAGAAAATGTAGCCCATTACCACATGT  
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTIONCACAGAGGGAGAGAAAAGATGTGT  
 ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA  
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC  
 AGGTCATTTACAATTGGGAGATTTCAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTG  
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG  
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA  
 AATACCCATTGGCTATGCCACTTGAAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT  
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG  
 AAATGTGTCAATCAATTTCTGGATTATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG  
 GTCACCTTCATTCTGGACACAGTTGGATCAATACTGATTAAAGTAGAAAATCCAAGCTTTGCTT  
 GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

**FIGURE 212**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGGVYLGNYPPFKDRISWAGDLDDKSDASINIEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNSKRDTGCTSESLSPPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHS  
GHHSKINKSESVVYADIRKN

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

**FIGURE 213**

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTGCAGCAGTGACTGCCCGGGCTGCCGCC  
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC  
 TCTCGGCCACGGCTGGGTGCGGGGCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC  
 TGGCAGGTGGGCTGAGGGGCGCGGGCCCCGGCGCAGTCCCCGCGGCCCCGACCCTGAGGCG  
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC  
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
 TCAAGGATGAGGTGGGCGCACCCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC  
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT  
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG  
 CAGGGAACTGGATCTTGATATTCAGTACAACATTATGTTCCCGAATTCAGAAAAAGAA  
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTGCG  
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
 TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAGTAATGAAAAGAATGATTTT  
 ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGAATTCAAAACCTGGCAAGAA  
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAAT  
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA  
 ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAATATTTGGA  
 CTATATGCAGAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
 CAGTGATTACAATAGAGCAAGGTAAATGAATACCTTCTGCTGTGCTAGCTATATCGCATC  
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC  
 CACATTTTGGGAGCTTTTCTACATGCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA  
 TGTTTATAAAGTAAAAAA



**FIGURE 214**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAAPGGLASSCGRRGVHQRAGLPPLGHWVGGLGLGLGLALGVKLAGGLRG  
AAPAQSPAAPDPEASPLAEPPQEQLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA  
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD  
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF  
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN  
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

**FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG  
 AGGCTGGTGGGAAGAAGCCGAG**ATG**GCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCGAGCGGCTGCCGGGCCGGGACT  
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT  
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACCTCCGGAAGCGGGGCTCACTGCTCT  
 GGAACCAGCAGGATGGTACCTTTGCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
 TGGAGTCGCACCTGTTCGGACCAGCTGACCCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
 GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG  
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG  
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCTCTGTTCTCATGATGTCAGG  
 AGCGCCAGACACCGGGGGCCAGGTTGGGGTGGGGGTGGGGTGGTGGTGGGGTAGTGGCC  
 TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTAAAAACATCGACGATACATTGAAATGTG  
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
 TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTACAGAAACCCAAG  
 GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
 TAAACTGTCCCCCAGATCGACACGCAAAAAAAAA

**FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIIPRRPGALDGLEA  
GGYVSSFVPACSLVESHLSQDLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ  
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEOKSFFAKYWMYIIPVVFLMMSGAPDTGGQ  
GGGGGGGGGGGSLCCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGAGCCACAGCGGGGAGGGTGCCCTGGCGGCCT  
 GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTCGTCCGGGGGCCACC  
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC  
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC  
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
 CTCTATAAACTCTACCAGCATTACTTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
 TGGCCTTGCCCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTTGGATTGGCTGGGTC  
 GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT  
 CAAGACTACTTTGTGTCTGTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGGAGAAGTATGACC  
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGACCGCCGC  
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCCT  
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
 CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTTTCATGTTGACTTT  
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT  
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA  
 GAGCAGGCTGGTGTACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT  
 CCTGTCTCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTCAGCATTGTCTCTG  
 CTGTGATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCGTGGAAGGCATGATGCT  
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTGTAACCCCACTCCAG  
 GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT  
 GACTGACTTTTGTGACTGTCTGTGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA  
 ATAAACACTTTTAAATGATCAAAAAAAAAA

**FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
VAAEAVASWIGLGPVAPFVAAIPLLAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGII FSSFMAASLLGSSLYRIATSKRYHLQ  
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET  
EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA  
ELRVFPSPTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
314-330, 343-359, 379-394, 410-430

**FIGURE 219**

GCGACGCGCGGGGGCGGCGAGAGGAAACGCGGCGCCGGGCCGGGCCCTGGAG**ATG**  
 GTCCCCGCGCGCGGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA  
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTTCGATACA  
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCA  
 GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC  
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG  
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
 CCATCCCAGTCAATGTCAACAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
 TGG**TAGA**AAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
 AGGAATTTTGCTACTTGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA  
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG  
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
 CACCTGGCTCCAGCCTCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
 AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTAGCAATAAA  
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 220**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ  
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF  
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

**Signal peptide:**

amino acids 1-20



**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACTTGCACTGCTGTGTGGGCTGGTGGTGA  
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG  
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG  
AGGCCAACCCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC  
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT  
TTATCTCAACGCTATTGTTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC  
CGAA**TAA**AAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
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**FIGURE 222**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538  
><subunit 1 of 1, 116 aa, 1 stop  
><MW: 12910, pI: 6.41, NX(S/T): 1  
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPHYGCHCGLGGRGQPKDATDW  
CCQTHDCCYDHLKTQCGGIYKDNKNKSSIHCMDSLQRYCLMAVFNVIIYLENEDSE

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGCCCCAGGGGGCCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTACGACCACTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACCTCACCCGTGGGTGCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAA

**FIGURE 224**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLKSVQVK  
LGDSWDVKLGALGGNTQEVTLPGEYITKVFAFQAFLRGMVMYTSKDRYFYFGKLDGQISS  
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYANSFVGR

**Signal peptide:**

amino acids 1-22

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**FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAATGGGTGCTCATCACGGGAACGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCAAATTGGCTGGAAGAATACATCATGTTTTTCGATAAGAAAGAAATGTAGGATCCAGTT  
 TTTTTTTTAAACGCCCCCTCCCCACCCCCCAAAAAAAGCTGAAAGATGCAAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
 TATTTGTTCTTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT  
 CCCAAGGGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG  
 ACAGGGGCTGTCATGCAACTGGCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA  
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA  
 TATCTGCTGGTGTCTTAGGTTTGTCCCTTCGTATAACAGCCTTCAAAAACCTAAGTATAAT  
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
 TCTCCTATTTTCTTAACAATAACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCAGGAGCTGCTGAGTTT  
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATCCAAGACTGCCGCAACC  
 TGGAACTTTTGGACCTGGGATATAAACCGGATCCGAAGTTTLAGCCAGGAATGTCTTTGCTGGC  
 ATGATCAGACTCAAAGAATTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT  
 TTTTCCAAGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGAATAAAATCAGTGTATAG  
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC  
 GAAGCTTTTCACTGGACCCAGTGTTTTTCCAGTGTGTCCGAATCTGCAGCGCCTCAACCTGGA  
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA  
 TCAGTCTTGTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAAACTGGCTG  
 AAAAGTTTTAAAGGCTAAAGGAGAATACAATTATCTGTGCCAGTCCCAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT  
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCGAGGCCGAAGCAT  
 GAGAGCAAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCCGGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG  
 TGCTCGTCATCTGCTGGTTATCTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAG  
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAGACAGTCCCTAAAGCAAAAT  
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAAACCCACCAACACGGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
**TGA**ACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTGCTTTATTGAACCT  
 TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG  
 CAAGATCCTTCCCTGTCCGTTTTAGTGCATTACATAACTGGTCATTTTCTCTCATACATA  
 ATCAACCCATTGAAATTTAAATACACCAATCAATGTGAAGCTTGAACCTCCGGTTTTAATATAA  
 TACCCTATTGTATAAGACCTTTACTGATTCCATTAATGTCGATTTGTTTTAAGATAAAAAC  
 TCTTTCATAGGTAAAAA

**FIGURE 226**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301  
><subunit 1 of 1, 513 aa, 1 stop  
><MW: 58266, pI: 9.84, NX(S/T): 4  
MGFNVIRLLSGSAVALVIAPT VLLTMLSSAERGCPKGCRCGKMGVYCESQKLQEIPSSISAG  
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF  
LNNTRFPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL  
DLGYNRIRSLARNVFAGMIRLKEHLHNNQFSKLNALFPRLVSLQNLYLQWNKISVIGQTM  
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLTFIQEILDSWISLNDISLA  
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA  
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI  
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLN  
GTGPCTYNKSGSRECEV

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT  
 TAAAT**ATG**TCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG  
 TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
 AAATTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
 ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGTCTGTGGAGACTTGGACTCTATTTATGG  
 GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
 ATCCTGTTCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
 AAAACAACCT**TGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATCCCA  
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA  
 GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG  
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
 AACCAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
 CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
 CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
 CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG  
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
 CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTGAACAAAACAAT  
 AAACATCAATAGATATCTAAAAA

**FIGURE 228**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVA  
ALLCGAVVLCLQCWLRPRIDSHRRTMAVFVAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP  
VPAPCFGPLGSPPPYEEIVKTT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

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**FIGURE 229**

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA  
 GCTCTCGCTGCGTCGCCCGGCTCAGAAGCTCCGTGGCGGCGGCAGCCGTGACGAGAAGCCC  
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCTTTTAACT  
 CCTCTTTCAAACCTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG  
 ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGC  
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTTA  
 CAATCTCAAGAAAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT  
 TGGGGATTGATGTTACTGCACTATACTTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAATACTAGACTTAAGCAAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAAAT  
 GCTGTCTCTTCTGGATGACATTTTGAACGATTGGTGAAAGCTGGAGAACAAAGTTGACTATAT  
 TGTGTGAATGGCTCAGCAGCCAAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA  
 CCACAAATAAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATAGCTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAAC  
 TCTAATTCGTACATAAAAAATTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG  
 CTGTACTATGCTCTTAAAGAGAATTTGGTAACCTGGTTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATT  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAA  
 TCATTCTGTCATTTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAAATGTG  
 CTTATTGTACTATATTTTGTATTCCAAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTGCACTATCCTTCAGAATAACTGA  
 AGGTTAATTATTGTATATTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAATAATAGTT  
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTATGATGAGAGTAACAATA  
 AAGTATTCATGATTTTTTCACATACATGAATGTTCAATTTAAAAGTTTAAATCCTTTGAGTGTCT  
 ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGCTTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA  
 GGTACTTTTTGTGCTGCATTAAATTGCTTGGAAGTGTTAACATTATATATATAAGAGTATC  
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
 TTAATAAAGAACATTTAAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT  
 GTATATAGCACAGGGAACCTAATCTTGGGTAATCTAGTATAAAACAAATTATACTTTTTAT  
 TTAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT  
 CTCTATAGTAACTGCTTAAAGTGCAGCTAGCTTCTAGATTAGACTATATAGAATTTAGATAT  
 TGTATTGTTCTGCTATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAATA  
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTTCTCTCTCTGTA  
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT



**FIGURE 230**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
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**Important features of the protein:****Signal peptide:**

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**FIGURE 231**

CGCGGCCGGGCCGGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
 CATGCCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCCGGCCATGCT  
 TCCCGGGTGCCAATGCGCTGAGTGGAGACCTTCGGCCTTTTTCGACAGCTTCAGCCTTGCCG  
 GTGGATTGTAGCGCCTGGGCCCCACATCATGCCGCTGCCATCCCTCTGGACACAGCCCA  
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGGCT  
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTACCCACTGCC  
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
 AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG  
 AGGTCTCAGTGTCTGCCCTTACGACGCACAGTCAGGGCCGGGCATACAGTGGACCTCTCC  
 CACAACCTCATTACCCCTCTGTCGCCCAACCCACGAGGGCCGGCCTGCCTGCGGCCACCAT  
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGCCCC  
 TGGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCTATGGTCCGGGTGCCCTTCCGCGGG  
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
 TGGCTTCCGTGAGTACCGGGCCTGCAGGTCTTGACCTGTTCGGGCAACCCCAAGCTTAAC  
 TGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTTCGGGCACC  
 AACCTGGTGGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT  
 GGGCCAGGATGTGCGGTGCCGCGCCTGGTGGGGAGGGCACCTACCCCGAGGCCTGGCT  
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGCCCCACC  
 ATCTTGTGACAAATGGTGTGCCCCAGGGCCACATAACAGACTGCTGTCTTGGGTGCCCTCAG  
 GTCCCCGAGTAACCTTATGTTCAATGTGCCAACACCACTGGGGAGCCCCGAGGCCTATGTGGCA  
 GCGTCACCCAGGAGTTGTGGCCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
 AACCAAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCCTCCCTCAT  
 GCCTGGGCCGGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
 GTTCAGGTCCAATGGGCTGAGTGTCCCTTGGGGCCATGGGCCACTCAGGGGCGAGTT  
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT  
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTTCTCATGTGAC  
 AGATGGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCTGCGGGCAGTGGC  
 ATGACTGGAGCACAGCCTCCTGCCTCCAGCCCGGACCCAATGCACTTTCTTGTCTCCTCTA  
 ATAAGCCCCACCCTCCCCGCTGGGCTCCCCCTGCTGCCCTTGCTGTTCCTCCCATTAGCACA  
 GGAGTAGCAGCAGCAGGACAGGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT  
 GTGCGGCATGGGCTAAGTCACCTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT  
 CCAGCCTAGCCAGTTTCTCACCCTGGGTGGGGTCCCCAGCATCCAGACTGGAACCTACC  
 CATTTTCCCCCTGAGCATCCTCTAGATGCTGCCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA  
 TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTGAGTCCCCACTGGCCCTGAGCACGACAGC  
 CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGTCTATGC  
 TCTACCCCCAGGCGAGCATCTCAGCTTCCGAACCTGGGCTGTTTCTTAGTCTTCATTTTA  
 TAAAGTTGTTGCCTTTTAAACGGAGTGTCACTTTCAACCGCCTCCCTACCCCTGCTGGC  
 CGGGGATGGAGACATGTCAATTGTAAAAGCAGAAAAAGGTTGCATTGTGTTCACTTTGTAAAT  
 ATGTCTGCGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC  
 CCATCATCTATCTAACCGTCTTGTGATTTAATAAACACTATAAAAGGTTTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 232**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCTGTGGGTCTGAGG  
 GGACCAGAAGGGTGAGTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCA  
 AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCTGCT  
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCAC  
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCC  
 TCTAGTCTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA  
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAAACCAGACCCCTGACCATTATACTCTCC  
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
 CTTTGAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGAACTAGACATTCTTC  
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT  
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTACT  
 GTACTAGTCTTGCTGGTGCAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT  
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTT  
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGTATTTAATGTATTT  
 ATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
 AGCAGGTGATGTATTTTTATACAGTAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT  
 AGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGAATT  
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT  
 CTTCAGCCAGGAATCCTACAGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA  
 CCAAAAAAAAAAAAAAAAAA

**FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 29667, pI: 8.76, NX(S/T): 0  
MRQFPKTSFDISPEMSFSIYSLQVPVPG LTCWALTAEPGWGQNGATTTCATNSHSDSELRP  
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVIATNL  
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP  
DHYTLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG  
ELDILLQWMEETE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGAGAGGCTTTTGCCG  
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGCG  
CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG  
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGACA  
GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT  
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG  
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG  
GCTGGTGTATTGGCCAGTTTTTAGCCAATCCAACCTGACCTAGTGAAGGTTTCAAGTCAAAT  
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGCGATTCGTGGTGTACATCATGCATTTG  
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
AGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTTATGATACAGTGAAACACTACTTGGT  
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA  
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT  
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC  
CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
TTTTAA

**FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPPLDLTKTRLQMGEAALARLGDGA  
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEH  
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFKILAEGGI  
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP  
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT  
YEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

**FIGURE 237**

CGGACGCGTGGGCGCGGGACGCCGCGAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
 GCCTGAAGTCGCGCGTGGGCGTTTGTAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
 TTAAGAAGTAAAA**ATG**GCGAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTTACAGGC  
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
 TCACACATGTGGTGTATTTTCCACATTTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC  
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC  
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA  
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCT**TCAG**ATCAC  
 TTCTTAAGTCACATTTTCCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT  
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTT  
 TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTCATTGCATAGACTGTTAATATGTA  
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA  
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT  
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG  
 CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT  
 AAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCAGCTACCTGGGAGGC  
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGCGAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
 TGCACCTCTAGCCTGGGGGAGAAAGTGAACCTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
 TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTGGTAAAGA  
 AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC  
 AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCTCTAATATGACTTTTATGTGAGAA



**FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVGILFFTGWIMIDAADVYPKPEQLNHAFHTCG  
 VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
 NTDVYPGLAVFFQNALIFFSTLIYKFGRTTEELWT

**Important features:****Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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**FIGURE 239**

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
 CTGGCGGGCCCGCAACACTCCGTCTCACCTCTGGGCCCCTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT  
 GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCCTTCACCTGGACAG  
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
 TGTATTATCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC  
 AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
 GCTTTGAAGACCGCATGATCATGAGTCTGTGAAAAACAATGTGGGCAGAGGCCATAACATC  
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGTGGTGG  
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG  
 GGGAGTTCCTACGAAAACAACTGGGCTTCCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
 CCTCAGGGGTAAAAGCCCCCTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG  
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC  
 TGTGGCTCTTCTCAGCCAGGGGCCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCCG  
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGCACGC  
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCTCCCACAGCACATCTACCCGAAGACC  
 AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGG  
 ACTGCTGACGGCTGGTCCTGAGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTA  
 TTTTGTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAAA

**FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:****Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT  
 CCAGAAACCCATGATACCCCTACTGAACACCGAATCCCCTGGAAGCCACAGAGACAGAGACA  
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC  
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCCTCTAGTCCTCAAATCCCAGTCCC  
 CTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCC  
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA  
 GCCTCTTACCCTGAGTGTGGAAACAATGCCAGTCGCCATCGATATTGACACAGACAGTGT  
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC  
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTGCCCCCTACCCCTGTATCTG  
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC  
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC  
 ATTATGACTCTGATTCCATGACAGCTTGAGTGAGGCTGCTGAGAGGCTCAGGGCCTGGCT  
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG  
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTCCGCTACAATGGCTCGCTCACAACCTCCCCCT  
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCAGATTTCAATGGAACAGCT  
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA  
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
 CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA  
 AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATTAAATTCCTTCTCAGATACCA  
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG  
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCTGGACATCTCTTAGAGAG  
 GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA  
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGCAGGG  
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA  
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTTGTATCAATA  
 TATTTGGAAATTAAAGTTCTGACTTT

**FIGURE 242**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812  
><subunit 1 of 1, 337 aa, 1 stop  
><MW: 37668, pI: 6.27, NX(S/T): 1  
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPDLP  
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQ  
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH  
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLL  
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF  
IARKIRKKRLENRKSVVFTSAQATTEA

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

[illegible][illegible]

**FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLSLIPLTQM  
 LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGILNVQQQLHPLVLPFVFTQLGAQGTILSSEE  
 LPQIFTSLLIHSFLPGGILPSTSQAGANPDVQDGSPLPAGGAGVNPATQGTTPAGRLPTPSG  
 TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

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**FIGURE 245**

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG  
 GAGCCAGACGCTGACCACGTTCTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCG  
 GCAGCCGGGAGCC**ATG**CGACCCCAGGGCCCCGCCGCCTCCCCGCAGCGGCTCCGCGGCCTCC  
 TGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGACCTGTATAATGGAATGTGCTTACAAGG  
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG  
 GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAG  
 GAGTCTGGACACCCAACCTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT  
 TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTGT  
 TCAGTGGCTCACTTCGGCTAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC  
 AATGGAGCTGAATGTTCAAGACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCAAGGAAG  
 CCCTGAAATGAATCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAA  
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA**  
**AAT**GCCTTTAATTTTCATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACCTAAAT  
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
 CCAAAGTGTGATTTCACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGT  
 GTTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
 TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA  
 TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT  
 AAAAAATTATTTCCAACA



**FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEGKEGCLRESFEESWTPNYKQCSWSSLNYGIDLKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217